

GenCore version 5.1.6
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4 nucleic - nucleic search, using sw model

in on: April 19, 2004, 15:54:48 ; Search time 0.001 Seconds
(without alignments)
1.176 Million cell updates/sec

tle: US-10-024-396-3-COPY

fect score: 28

quence: 1 cgggcctacgtacagggagtcagg 28

oring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

arched: 2 seqs, 21 residues

tal number of hits satisfying chosen parameters: 4

imum DB seq length: 0

iximum DB seq length: 2000000000

et-processing: Minimum Match 0%

Maximum Match 100%

Listing first 2000 summaries

atabase : esdb:*

EST

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7.4	26.4	11	1	BM395068
2	7	25.0	10	1	BM393918
3	7	25.0	11	1	BM395068
4	6.4	22.9	10	1	BM393918

ALIGNMENTS

RESULT 1
BM395068/c

LOCUS 11 bp mRNA linear EST 17-JAN-2002

DEFINITION 50072-2-7-D04.r.1 Chilcoat/Turkewitz cDNA (large fraction)

ACCESSION BM395068

VERSION BM395068

KEYWORDS EST.

SOURCE Tetrahymena thermophila

ORGANISM Tetrahymena thermophila

REFERENCE Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymena; Tetrahymena.

AUTHORS Frankel, J. and Klobutcher, L.

TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells

JOURNAL Unpublished (2002)

COMMENT Contact: Turkewitz AP
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Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu

Seq primer: T3.

Location/Qualifiers

1. .11

/organism="Tetrahymena thermophila"

/mol_type="mRNA"

/strain="CU428.1"

/db_xref="taxon:5911"

/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"

/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 26.4%; Score 7.4; DB 1; Length 11;

Best Local Similarity 88.9%; Pred. No. 0;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GGGCCCTAC 10
|||||

Db 11 GGGCCCGAC 3
|||||

RESULT 2

BM393918 10 bp mRNA linear EST 17-JAN-2002

LOCUS 50072-2-11-H06.r.1 Chilcoat/Turkewitz cDNA (large fraction)

DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM393918

VERSION BM393918.1 GI:18193971

KEYWORDS EST.

SOURCE Tetrahymena thermophila

ORGANISM Tetrahymena thermophila

REFERENCE Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymena; Tetrahymena.

AUTHORS Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J. and Klobutcher, L.

TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells

JOURNAL Unpublished (2002)

COMMENT Contact: Turkewitz AP
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Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu

Seq primer: T3.

Location/Qualifiers

1. .10

/organism="Tetrahymena thermophila"

/mol_type="mRNA"

/strain="CU428.1"

/db_xref="taxon:5911"

/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"

/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 CGGGCCCC 8
|||||

RESULT 3

BM395068 11 bp mRNA linear EST 17-JAN-2002

LOCUS 50072-2-7-D04.r.1 Chilcoat/Turkewitz cDNA (large fraction)

DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM395068

VERSION BM395068.1 GI:18195121

WORDS

Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 11)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,
Frankel, J., and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES

1..11
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/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match

Best Local Similarity 25.0%; Score 7; DB 1; Length 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGGGCCC 7
|||||||
5 CGGGCCC 11

MULT 4

193918/c
TUS
INITIATION
50072-2-11-H06.r.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.

SESSION

BM393918
BM393918
BM393918.1 GI:18193971

WORDS

Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 10)

Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,
Frankel, J., and Klobutcher, L.

EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)

JOURNAL

Unpublished (2002)

MENT

Contact: Turkewitz AP
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Tel: 773 702 4374
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Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES

1..10
Location/Qualifiers
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 22.9%; Score 6.4; DB 1; Length 10;
Best Local Similarity 87.5%; Pred. NO. 0;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGCCCTA 9
|||||||
Db 8 GGGCCCGA 1

Search completed: April 19, 2004, 15:54:48
Job time : 0.001 secs

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4 nucleic - nucleic search, using sw model
in on: April 19, 2004, 14:25:24 ; Search time 0.001 Seconds
(without alignments)
208.040 Million cell updates/sec

File: US-10-024-396-3-COPY
Project score: 28
Sequence: 1 cgggcccctacgtgtacagggagtcagg 28

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Aligned: 288 seqs, 3715 residues
Total number of hits satisfying chosen parameters: 576

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 301 summaries

Database: rgedb:* GenEmbl

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
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3	18.2	65.0	25	1	AX690107	ACCESSION:AX690107
4	18.2	65.0	25	1	AX690108	ACCESSION:AX690108
5	17.8	63.6	25	1	AX690105	ACCESSION:AX690105
6	17.8	63.6	25	1	AX690106	ACCESSION:AX690106
7	17.6	62.9	25	1	AX690111	ACCESSION:AX690111
8	16.8	60.0	25	1	AX690104	ACCESSION:AX690104
9	16.6	59.3	25	1	AX690112	ACCESSION:AX690112
10	14.4	51.4	17	1	AX688603	ACCESSION:AX688603
11	14.4	51.4	17	1	AX688604	ACCESSION:AX688604
12	14.2	50.7	21	1	AX165205	ACCESSION:AX165205
13	13.8	49.3	17	1	AX688605	ACCESSION:AX688605
14	13.8	49.3	17	1	AX688606	ACCESSION:AX688606
15	13.8	49.3	17	1	AX688607	ACCESSION:AX688607
16	13.8	49.3	17	1	AX688608	ACCESSION:AX688608
17	13.4	47.9	17	1	AX688602	ACCESSION:AX688602
18	13.4	47.9	18	1	AX058208	ACCESSION:AX058208
19	13.4	47.9	18	1	AX143261	ACCESSION:AX143261
20	13.4	47.9	20	1	AX449606	ACCESSION:AX449606
21	13.2	47.1	19	1	ED088466	ACCESSION:ED088466
22	13.2	47.1	19	1	AB065243	ACCESSION:AB065243
23	13.2	47.1	20	1	AX294766	ACCESSION:AX294766
24	12.8	45.7	17	1	AX688609	ACCESSION:AX688609
25	12.8	45.7	17	1	E32811	ACCESSION:E32811
26	12.4	44.3	17	1	AX688601	ACCESSION:AX688601
27	12.4	44.3	18	1	AX711184	ACCESSION:AX711184
28	12.4	44.3	19	1	AR016655	ACCESSION:AR016655
29	12.4	44.3	19	1	AX110278	ACCESSION:AX110278
30	12.2	43.6	17	1	AX413938	ACCESSION:AX413938
31	12.2	43.6	17	1	AX688610	ACCESSION:AX688610
32	12.2	43.6	17	1	AX783828	ACCESSION:AX783828
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36	12	42.9	17	1	AX688599	ACCESSION:AX688599
37	12	42.9	17	1	BD246816	ACCESSION:BD246816
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45	11.2	40.0	16	1	AR091341	ACCESSION:AR091341
46	11.2	40.0	16	1	AR118047	ACCESSION:AR118047
47	11.2	40.0	16	1	AR127765	ACCESSION:AR127765
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160	8.4	30.0	10	1	AR167743	ACCESSION:AR167743	C 233	8	28.6	10	1	AX632794	ACCESSION:AX632794
161	8.4	30.0	10	1	AR178738	ACCESSION:AR178738	C 234	8	28.6	10	1	I11566	ACCESSION:I11566
162	8.4	30.0	10	1	AR178841	ACCESSION:AR178841	C 235	8	28.6	10	1	I14185	ACCESSION:I14185
163	8.4	30.0	10	1	BD251252	ACCESSION:BD251252	C 236	8	28.6	10	1	I24587	ACCESSION:I24587
164	8.4	30.0	10	1	E29627	ACCESSION:E29627	C 237	8	28.6	10	1	AX235321	ACCESSION:AX235321
165	8.4	30.0	10	1	E38733	ACCESSION:E38733	C 238	8	28.6	10	1	AX711182	ACCESSION:AX711182
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167	8.4	30.0	10	1	AR205443	ACCESSION:AR205443	C 240	7.8	27.9	10	1	AX472098	ACCESSION:AX472098
168	8.4	30.0	10	1	AR220135	ACCESSION:AR220135	C 241	7.8	27.9	10	1	I16095	ACCESSION:I16095
169	8.4	30.0	10	1	AR221524	ACCESSION:AR221524	C 242	7.8	27.9	10	1	AR301655	ACCESSION:AR301655
170	8.4	30.0	10	1	AR224308	ACCESSION:AR224308	C 243	7.8	27.9	10	1	AR301691	ACCESSION:AR301691
171	8.4	30.0	10	1	AR254226	ACCESSION:AR254226	C 244	7.8	27.9	10	1	AX470747	ACCESSION:AX470747
172	8.4	30.0	10	1	AR282432	ACCESSION:AR282432	C 245	7.8	27.9	10	1	AX470906	ACCESSION:AX470906
173	8.4	30.0	10	1	AR368339	ACCESSION:AR368339	C 246	7.8	27.9	10	1	AX470952	ACCESSION:AX470952
174	8.4	30.0	10	1	AX463121	ACCESSION:AX463121	C 247	7.8	27.9	10	1	AX471524	ACCESSION:AX471524
175	8.4	30.0	10	1	AX711090	ACCESSION:AX711090	C 248	7.8	27.9	10	1	AX471669	ACCESSION:AX471669
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177	8.4	30.0	10	1	BD001622	ACCESSION:BD001622	C 250	7.8	27.9	10	1	AX471796	ACCESSION:AX471796
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179	8	28.6	9	1	AX456625	ACCESSION:AX456625	C 252	7.8	27.9	10	1	AX624024	ACCESSION:AX624024

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253 7.8 27.9 11 1 AX624330
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277 7.8 27.9 11 1 BX124405
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284 7.8 27.9 12 1 E38651
285 7.8 27.9 12 1 E64077
286 7.8 27.9 12 1 I23754
287 7.8 27.9 12 1 I35021
288 7.8 27.9 12 1 AR224412
289 7.8 27.9 12 1 AX073604
290 7.8 27.9 12 1 AX073609
291 7.8 27.9 12 1 AX105525
292 7.8 27.9 12 1 AX454105
293 7.8 27.9 12 1 AX454110
294 7.8 27.9 12 1 BD023278
295 7.8 27.9 25 1 AX690109
296 7.8 27.9 25 1 AX690110
297 7.8 27.9 25 1 AX690107
298 7.8 27.9 25 1 AX690108
299 7.8 27.9 25 1 AX690111
300 7.8 27.9 25 1 AX690112
301 7.6 27.1 10 1 AX096928
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ALIGNMENTS

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RESULT 1
LOCUS AX690109 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 2841 from Patent EP1281758.
ACCESSION AX690109
VERSION AX690109.1 GI:29412967
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 2841 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source 1. .25
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Query Match 66.4%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No.2.5;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GGCCTACGTGTACAGGAGTCCAG 27
| | | | | | | | | | | | | | | | | | | |
Db 1 GGCCTACGTGTACAGGAGTCTG 25

RESULT 2
LOCUS AX690110 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 2842 from Patent EP1281758.
ACCESSION AX690110
VERSION AX690110.1 GI:29412968
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 2842 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source 1. .25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 66.4%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No.2.5;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GGCCTACGTGTACAGGAGTCCAG 28
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Db 1 GGCCTACGTGTACAGGAGTCTG 25

RESULT 3
LOCUS AX690107 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 2839 from Patent EP1281758.
ACCESSION AX690107
VERSION AX690107.1 GI:29412965
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 2839 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 65.0%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No.3.1;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGCCTACGTGTACAGGAGTCC 25
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SULT 6					
690106					
CUS	AX690106	25 bp	DNA	linear	PAT 31-MAR-2003
FINITION	Sequence	2638	from Patent	EP1281758.	
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mdz12
JOURNAL Patent: EP 1281758-A 2836 05-FEB-2003;
Aeomica, Inc. (US)
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source
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/mol_type="unassigned DNA"
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Best Local Similarity 90.0%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
/ 3 GGCCTACGTGTACGGAG 22
6 GGCCTACGTGTGCGAG 25

RESULT 9
LOCUS AX690112 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 2844 from Patent EP1281758.
ACCESSION AX690112
VERSION AX690112.1 GI:29412970
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 2844 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 59.3%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 7.5;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
/ 6 CCTACGTGTACGGAGTCCAG 28
1 CCTACGTGTGCGAGTGTGG 23

RESULT 10
LOCUS AX688603 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1335 from Patent EP1281758.
ACCESSION AX688603
VERSION AX688603.1 GI:29411305
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 1335 05-FEB-2003;
Aeomica, Inc. (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 51.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 11;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 GGCCTACGTGTACAG 18
DB 2 GGCCTACGTGTGCAG 17

RESULT 11
LOCUS AX688604 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1336 from Patent EP1281758.
ACCESSION AX688604
VERSION AX688604.1 GI:29411306
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 1336 05-FEB-2003;
Aeomica, Inc. (US)
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/mol_type="unassigned DNA"
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Best Local Similarity 93.8%; Pred. No. 11;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 GGCCTACGTGTACAG 18
DB 1 GGCCTACGTGTGCAG 16

RESULT 12
LOCUS AR165205 21 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 19 from patent US 6274708.
ACCESSION AR165205
VERSION AR165205.1 GI:16238680
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Hilton, D.James.
TITLE Mouse interleukin-11 receptor
JOURNAL Patent: US 6274708-A 19 14-AUG-2001;
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/organism="unknown"
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Query Match 50.7%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 19;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 10 CGTGTACGGAGTCCAG 28
DB 3 CCTGTACTTGGAGTCCAG 21

RESULT 13
LOCUS AX688605 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1337 from Patent EP1281758.

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SESSION AX688605 49.3%; Score 13.8; DB 1; Length 17;
SION AX688605.1 GI:29411307 17 bp DNA linear PAT 31-MAR-2003
TRACE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL mdz12
PATENT: EP 1281758-A 1337 05-FEB-2003;
AECOMICA, Inc. (US)
FEATURES
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Query Match 49.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 15;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCTACGTGTACAGGAG 22
Db 1 CCTACGTGTACAGGAG 17

RESULT 16
AX688608 17 bp DNA linear PAT 31-MAR-2003
LOCUS Sequence 1340 from Patent EP1281758.
DEFINITION AX688608
ACCESSION AX688608.1 GI:29411310
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL mdz12
PATENT: EP 1281758-A 1340 05-FEB-2003;
AECOMICA, Inc. (US)
FEATURES
    Location/Qualifiers
    1..17
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"
Query Match 49.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 15;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGGAGT 23
Db 1 CTACGTGTACAGGAGT 17

RESULT 17
AX688602 17 bp DNA linear PAT 31-MAR-2003
LOCUS Sequence 1334 from Patent EP1281758.
DEFINITION AX688602
ACCESSION AX688602.1 GI:29411304
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL mdz12
PATENT: EP 1281758-A 1334 05-FEB-2003;
AECOMICA, Inc. (US)
FEATURES
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    /mol_type="unassigned DNA"
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SESSION AX688605 49.3%; Score 13.8; DB 1; Length 17;
SION AX688605.1 GI:29411307 17 bp DNA linear PAT 31-MAR-2003
TRACE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL mdz12
PATENT: EP 1281758-A 1337 05-FEB-2003;
AECOMICA, Inc. (US)
FEATURES
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"
Query Match 49.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 15;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCCTACGTGTACAGG 20
Db 1 GCCTACGTGTACAGG 17

RESULT 14
AX688606 17 bp DNA linear PAT 31-MAR-2003
LOCUS Sequence 1338 from Patent EP1281758.
DEFINITION AX688606
ACCESSION AX688606.1 GI:29411308
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL mdz12
PATENT: EP 1281758-A 1338 05-FEB-2003;
AECOMICA, Inc. (US)
FEATURES
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    1..17
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"
Query Match 49.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 15;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCCTACGTGTACAGGGA 21
Db 1 CCCTACGTGTACAGGGA 17

RESULT 15
AX688607 17 bp DNA linear PAT 31-MAR-2003
LOCUS Sequence 1339 from Patent EP1281758.
DEFINITION AX688607
ACCESSION AX688607.1 GI:29411309
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.

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Query Match          47.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 19;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

y 3 GGCCTACGTTGACA 17
   |||||
b 3 GGCCTACGTTGACA 17

RESULT 18
R058208/c
OCUS          AR058208          18 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION    Sequence 6 from patent US 5837694.
ACCESSION     AR058208
VERSION       AR058208.1 GI:5983785
KEYWORDS
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 18)
AUTHORS      Barrett,G.Leslie.
TITLE        Method for enhancing neurone survival and agents useful for same
JOURNAL      Patent: US 5837694-A 6 17-NOV-1998;
FEATURES     Location/Qualifiers
source       1..18
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match          47.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 21;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

y 12 TGTACAGGAGTCCA 26
   |||||
b 17 TGTACAGGAGTCCA 3

RESULT 19
R142361/c
OCUS          AR142361          18 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION    Sequence 6 from patent US 6174869.
ACCESSION     AR142361
VERSION       AR142361.1 GI:15102661
KEYWORDS
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 18)
AUTHORS      Barrett,G.Leslie.
TITLE        Method for enhancing neurone survival and agents useful for same
JOURNAL      Patent: US 6174869-A 6 16-JAN-2001;
FEATURES     Location/Qualifiers
source       1..18
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match          47.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 21;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

y 12 TGTACAGGAGTCCA 26
   |||||
b 17 TGTACAGGAGTCCA 3

RESULT 20
X449606/c
OCUS          AX449606          20 bp      DNA      linear      PAT 03-JUL-2002
DEFINITION    Sequence 35 from Patent WO210216.
ACCESSION     AX449606
VERSION       AX449606.1 GI:21698215
KEYWORDS
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SOURCE          synthetic construct
ORGANISM         synthetic construct
REFERENCE        1
AUTHORS          Padigaru,M., Mezes,P., Mishra,V., Burgess,C., Casman,S.,
                  Grosse,W.M., Alsobrook,J.P., Lepley,D.M., Gerlach,V.L.,
                  Macdougall,J.R. and Smithson,G.
TITLE           Proteins and nucleic acids encoding same
JOURNAL         Patent: WO 0210216-A 35 07-FEB-2002;
                  Curagen Corporation (US)
FEATURES        Location/Qualifiers
source         1..20
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Oligonucleotide primers"

Query Match       47.9%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 27;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 TACAGGGAGTCCAGG 28
   |||||
Db 17 TAGAGGGAGTCCAGG 3

RESULT 21
BD088466/c
LOCUS         BD088466          19 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION    A method of arraying genome clone.
ACCESSION     BD088466
VERSION       BD088466.1 GI:22634076
KEYWORDS      JP 2001321190-A/710.
SOURCE        synthetic construct
ORGANISM      synthetic construct
REFERENCE     1 (bases 1 to 19)
AUTHORS       Soeda,E.
TITLE        A method of arraying genome clone
JOURNAL      Patent: JP 2001321190-A 710 20-NOV-2001;
              THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
COMMENT      GENOTECHS
              OS Artificial Sequence
              PN JP 2001321190-A/710
              PD 20-NOV-2001
              PF 12-MAR-2001 JP 2001068285
              PI EIICHI SOEDA
              PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
              C12N15/00,
              CC Description of Artificial Sequence:Synthetic DNA PH Key
              CC Location/Qualifiers
              FT source 1..19
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              source 1..19
               /organism="synthetic construct"
               /mol_type="genomic DNA"
               /db_xref="taxon:32630"

Query Match       47.1%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 11 GTGTACAGGAGTCCAGG 28
   |||||
Db 19 GTGTACAGGAGTCCAGG 2

RESULT 22
AB069243/c
LOCUS         AB069243          19 bp      DNA      linear      SYN 21-MAY-2003
DEFINITION    Synthetic construct DNA, reverse primer for human Srs-L07033 at
```

```

1p36.
AB069243
AB069243.1 GI:15130047
synthetic construct
synthetic construct
artificial sequences.
1
Chen, Y.-Z., Hayashi, Y., Wu, J.G., Takaoka, E., Maekawa, K.,
Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H.,
Morohashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A.,
and Soeda, E.
A BAC-based STS-content map spanning a 35-Mb region of human
Chromosome 1p35-p36
Genomics 74 (1), 55-70 (2001)
21269192
PUBMED
11374902
2 (bases 1 to 19)
Horii, A.
Direct Submission
Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,
Tel: 81-22-717-8042, Fax: 81-22-717-8047)
Location/Qualifiers
1..19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
misc_feature
1..19
/notes="reverse primer for human STS sts-L07033 at 1p36
sts-L07033 obtained from clones B7H21, B7I21, B13SE5,
B196C16, B4SG17, B62G22, B8D9, B173B2, B89K16, B213F1,
Human BAC library RPC1-11"
Query Match 47.1%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

11 GTGTACAGGAGTCCAGG 28
19 GTGTAGGAGTGCACAGG 2

SULT 23
297476/c
CDS AX297476 20 bp DNA linear PAT 21-NOV-2001
FUNCTION Sequence 9238 from Patent WO0179548.
CDS AX297476
CDS AX297476.1 GI:17059167
WORDS
URCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
Barany, F., Zivni, M., Gerry, N.P., Pavis, R. and Kliman, R.
Method of designing addressable array for detection of nucleic acid
Sequence differences using ligase detection reaction
Patent: WO 0179548-A 9238 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Hypothetical Probe Sequence"
Query Match 47.1%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 30;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

10 CGTGTACAGGAGTCCAG 27
||||| |||||||

```

```

Db 20 CGTGTGTAGGAGTCCGG 3

RESULT 24
AX688609
LOCUS AX688609 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1341 from Patent EP1281758.
ACCESSION AX688609
VERSION AX688609.1 GI:29411311
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Shannon, M., Gu, Y. and Nguyen, C.T.
Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
Patent: EP 1281758-A 1341 05-FEB-2003;
Aemica, Inc. (US)
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 45.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TACGTGTACAGGAGT 23
||||| |||||||
1 TACGTGTGCAGCGAGT 16

Db 19 bp DNA linear PAT 31-JAN-2002
E32811
LOCUS E32811 19 bp DNA linear PAT 31-JAN-2002
DEFINITION Primer DNA and method for detecting mRNA encoding prostate
gland-specific antigen by using the same.
ACCESSION E32811
VERSION E32811.1 GI:18623941
KEYWORDS JP 2000069969-A/4.
SOURCE unidentified
ORGANISM unidentified
REFERENCE
1 (bases 1 to 19)
Nakagawara, H.
Primer DNA and method for detecting mRNA encoding prostate
gland-specific antigen by using the same
Patent: JP 2000069969-A 4 07-MAR-2000;
HITACHI CHEMICAL CO LTD, KK NIHON IDENSHI KENKYUJO
OS Unidentified
FN JP 2000069969-A/4
PD 07-MAR-2000
PF 28-AUG-1998 JP 1998243419
PR HIROKAZU NAKAGAWARA
PI C12N15/09, C12Q1/68, C12N15/00
PC C12N15/09, C12Q1/68, C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key
FT source
1..19
Location/Qualifiers
/organism="Unidentified".
FEATURES
source
1..19
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 45.7%; Score 12.8; DB 1; Length 19;
Best Local Similarity 87.5%; Pred. No. 33;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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6 CCTACGTTACAGGA 21
||| ||||| |||||
4 CCTGGTGTACAGGA 19

RESULT 26
ACUS 588601
DEFINITION Sequence 1333 from Patent EP1281758.
ACCESSION AX688601
VERSION AX688601.1 GI:29411303
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Shannon, M., Gu, Y. and Nguyen, C.T.
JOURNAL Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
FEATURES mdz12
PATENT: EP 1281758-A 1333 05-FEB-2003;
Aeonica, Inc. (US)
SOURCE Location/Qualifiers
1. 17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="caxon:9606"

Query Match 44.3%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 32;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

3 GGCCCTACGTGTAC 16
||||| ||||| |||||
4 GGCCCTACGTGTGC 17

RESULT 27
ACUS 711184/c
DEFINITION Sequence 484 from Patent EP1288296.
ACCESSION AX711184
VERSION AX711184.1 GI:29787565
KEYWORDS synthetic construct
ORGANISM synthetic construct
REFERENCE Draper, K.G., McSwiggen, J.A., Holecsek, J.J., Dudycz, L.W.,
AUTHORS Macejko, D.G. and Mamone, J.A.
TITLE Method and reagent for inhibiting HBV viral replication
JOURNAL Patent: EP 1288296-A 484 05-MAR-2003;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES Location/Qualifiers
1. 18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Nucleic acid clone fragments"

Query Match 44.3%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 36;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 CGGGCCCTACGTGT 14
||||| ||||| |||||
14 CGGGCCCGACGTGT 1

RESULT 28
ACUS R016655
DEFINITION Sequence 18 from patent US 5776762.
ACCESSION AR016655
VERSION AR016655.1 GI:3972932
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS North, M., Nishina, P., Noben-Trauth, K. and Naggert, J.
TITLE Obesity associated genes
JOURNAL Patent: US 5776762-A 18 07-JUL-1998;
FEATURES Location/Qualifiers
1. 19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 44.3%; Score 12.4; DB 1; Length 19;
Best Local Similarity 92.9%; Pred. No. 41;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGAGTCCAGG 28
||||| ||||| |||||
DB 6 ACAGGAGACCAGG 19

RESULT 29
ACUS AR110278
DEFINITION Sequence 30 from patent US 6114502.
ACCESSION AR110278
VERSION AR110278.1 GI:12826554
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS North, M., Nishina, P., Naggert, J. and Noben-Trauth, K.
TITLE Gene family associated with neurosensory defects
JOURNAL Patent: US 6114502-A 30 05-SEP-2000;
FEATURES Location/Qualifiers
1. 19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 44.3%; Score 12.4; DB 1; Length 19;
Best Local Similarity 92.9%; Pred. No. 41;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGAGTCCAGG 28
||||| ||||| |||||
DB 6 ACAGGAGACCAGG 19

RESULT 30
ACUS AX419938
DEFINITION Sequence 275 from Patent WO0198537.
ACCESSION AX419938
VERSION AX419938.1 GI:21524305
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Lyanichev, V., Allawi, H., Dong, F., Neri, B.P. and Vener, I.T.
TITLE Nucleic acid accessible hybridization sites
JOURNAL Patent: WO 0198537-A 275 27-DEC-2001;
FEATURES THIRD WAVE TECHNOLOGIES, INC. (US)
Location/Qualifiers
1. 17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

```

```

Query Match      43.6%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 36;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

2 GGGCCCTACGTGTACAG 18
|||||
1 GGACCTATGTCTACAG 17

RESULT 31
LOCUS      188610
DEFINITION      Homo sapiens
ACCESSION      AX698610
VERSION      AX698610.1 GI:29411312
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE
AUTHORS      Guo, J.
TITLE      Human prostate cancer candidate protein 1
JOURNAL      Patent: WO 03050284-A 2304 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
    Query Match      43.6%; Score 12.2; DB 1; Length 17;
    Best Local Similarity 82.4%; Pred. No. 36;
    Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

    QY      5 CCTACGTGTACAGGGA 21
    DB      17 CCTACGTATTAAGAGA 1

RESULT 32
LOCUS      783828/c
DEFINITION      Homo sapiens
ACCESSION      AX783828
VERSION      AX783828.1 GI:32951677
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE
AUTHORS      Guo, J.
TITLE      Human prostate cancer candidate protein 1
JOURNAL      Patent: WO 03050284-A 2159 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
    Query Match      43.6%; Score 12.2; DB 1; Length 17;
    Best Local Similarity 82.4%; Pred. No. 36;
    Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

    QY      9 ACGTGTACAGGAGTCC 25
    DB      1 ACGTGTGCAGGAGTCC 17

RESULT 33
LOCUS      AX783973/c
DEFINITION      Homo sapiens
ACCESSION      AX783973
VERSION      AX783973.1 GI:32951822
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE
AUTHORS      Guo, J.
TITLE      Human prostate cancer candidate protein 1
JOURNAL      Patent: WO 03050284-A 2304 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
    Query Match      43.6%; Score 12.2; DB 1; Length 17;
    Best Local Similarity 82.4%; Pred. No. 36;
    Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

    QY      5 CCTACGTGTACAGGGA 21
    DB      17 CCTACGTATTAAGAGA 1

RESULT 34
LOCUS      AR066781/c
DEFINITION      Sequence 129 from patent US 5851760.
ACCESSION      AR066781
VERSION      AR066781.1 GI:5998003
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE
AUTHORS      Evans, G.A. and Smith, M.W.
TITLE      Method for generation of sequence sampled maps of complex genomes
JOURNAL      Patent: US 5851760-A 129 22-DEC-1998;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
    Query Match      43.6%; Score 12.2; DB 1; Length 18;
    Best Local Similarity 82.4%; Pred. No. 41;
    Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

    QY      11 GTGTACAGGAGTCCAG 27
    DB      18 GTGAAAGGAGTCCGG 2

RESULT 35
LOCUS      AR083092
DEFINITION      Sequence 6 from patent US 5976803.
ACCESSION      AR083092
VERSION      AR083092.1 GI:10009882
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE
AUTHORS      Week, K.D.
TITLE      Genetic test for equine severe combined immunodeficiency disease
JOURNAL      Patent: US 5976803-A 6 02-NOV-1999;

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FEATURES
source
1. .18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 43.6%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 41;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

12 TGTACAGGGAGTCCAGG 28
|||||
1 TCTACAGGGAGTCCAGG 17

RESULT 36
LOCUS AX688599 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1331 from Patent EP1281758.
ACCESSION AX688599
VERSION AX688599.1 GI:29411301
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
PATENT: EP 1281758-A 1331 05-FEB-2003;
AUTHORS Aeomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 42.9%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3 GGCCCTACGTGT 14
|||||
6 GGCCCTACGTGT 17

RESULT 37
LOCUS AX688600 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1332 from Patent EP1281758.
ACCESSION AX688600
VERSION AX688600.1 GI:29411302
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
PATENT: EP 1281758-A 1332 05-FEB-2003;
AUTHORS Aeomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 42.9%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3 GGCCCTACGTGT 14
|||||
6 GGCCCTACGTGT 17

RESULT 38
LOCUS BD246816 16 bp DNA linear PAT 17-JUL-2003
DEFINITION Genotyping cytochrome expression.
ACCESSION BD246816
VERSION BD246816.1 GI:33056586
KEYWORDS JP 2002533136-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 16)
AUTHORS Paulussen, A.D.C. and Armstrong, M.
TITLE Genotyping cytochrome expression
JOURNAL Patent: JP 2002533136-A 2 08-OCT-2002;
COMMENT JANSSEN PHARMACEUTICA NV
OS Artificial Sequence
PN JP 2002533136-A/2
PD 08-OCT-2002
PF 22-DEC-1999 JP 2000591220
PR 23-DEC-1998 GB 9828619.8
PI AIMEE DYMENE CATHERINE PAULUSSEN, MARTIN ARMSTRONG PC
C12N15/09, C12Q1/02, C12Q1/68, G01N33/53, G01N33/566, C12N15/00 CC
Description of Artificial Sequence: primer
FH Key Location/Qualifiers
FT source 1. .16
/organism="Artificial Sequence".
FEATURES
source
1. .16
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 42.1%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

13 GTACAGGGAGTCCAG 27
|||||
2 GTACAGGGAGTCCAG 16

RESULT 39
LOCUS AX026612 16 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 2 from Patent WO0039332.
ACCESSION AX026612
VERSION AX026612.1 GI:10187786
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Paulussen, A.D. and Armstrong, M.
TITLE Genotyping cytochrome expression
JOURNAL Patent: WO 0039332-A 2 06-JUL-2000;
COMMENT JANSSEN PHARMACEUTICA NV (BE); PAULUSSEN AIMEE DYMENE CATHER (BE); ARMSTRONG MARTIN (GB)
FEATURES
source
1. .16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"

Query Match 42.1%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 39;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

13 GTACAGGAGTCCAG 27
|||||
2 GTACAGGAGACAG 16

SULT 40
711182/c
CUS
FINITION Sequence 482 from Patent EP1286296.
CESSION AX711182
RSION AX711182.1 GI:29787563
YWORDS
URCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Draper,K.G., Mcswiggen,J.A., Holecsek,J.J., Dudycz,L.W.,
Macejak,D.G. and Mamone,J.A.
TITLE Method and reagent for inhibiting HBV viral replication
JOURNAL Patent: EP 1286296-A 482 05-MAR-2003;
RIBOZYME PHARMACEUTICALS, INC. (US)
ATTRES Location/Qualifiers
source 1. 17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Nucleic acid clone fragments"
Query Match 40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 55;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2 GGGCCCTACGTGT 14
|||||
13 GGGCCCGACGTGT 1

SULT 41
001333
CUS
FINITION Sequence 23 from patent US 5739027.
CESSION AR001333
RSION AR001333.1 GI:3963400
YWORDS
URCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kamb,A.
TITLE MSL1E1.beta. gene
JOURNAL Patent: US 5739027-A 23 14-APR-1998;
ATTRES Location/Qualifiers
source 1. 16
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 40.0%; Score 11.2; DB 1; Length 15;
Best Local Similarity 81.2%; Pred. No. 54;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

10 CGTGTACAGGAGTCC 25
|||||
1 CGTGTCCAGGAAGCCC 16

SULT 42
037513
CUS
FINITION Sequence 23 from patent US 5801236.
CESSION AR037513
RSION AR037513.1 GI:5953369
YWORDS
URCE Unknown.

```

```

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kamb,A.
TITLE Probes for MTS1 gene and polynucleotides encoding mutant MTS1 genes
JOURNAL Patent: US 5801236-A 23 01-SEP-1998;
ATTRES Location/Qualifiers
source 1. 16
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 54;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 CGTGTACAGGAGTCC 25
|||||
Db 1 CGTGTCCAGGAAGCCC 16

RESULT 43
AR062793
LOCUS
DEFINITION Sequence 23 from patent US 5843756.
ACCESSION AR062793
VERSION AR062793.1 GI:5990484
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Stone,S., Jiang,P. and Kamb,A.
TITLE Mouse MTS1 gene
JOURNAL Patent: US 5843756-A 23 01-DEC-1998;
ATTRES Location/Qualifiers
source 1. 16
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 54;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 CGTGTACAGGAGTCC 25
|||||
Db 1 CGTGTCCAGGAAGCCC 16

RESULT 44
AR087871
LOCUS
DEFINITION Sequence 23 from patent US 5989815.
ACCESSION AR087871
VERSION AR087871.1 GI:10014634
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Skolnick,M.H., Cannon-Albright,L.A. and Kamb,A.
TITLE Methods for detecting predisposition to cancer at the MTS gene
JOURNAL Patent: US 5989815-A 23 23-NOV-1999;
ATTRES Location/Qualifiers
source 1. 16
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 54;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 CGTGTACAGGAGTCC 25
|||||

```

b 1 CGGTGCCAGGAGCC 16

RESULT 45
LOCUS AR091341 16 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 23 from patent US 5994095.
ACCESSION AR091341
VERSION AR091341.1 GI:10018096
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kamb,A.
TITLE MTS2 gene
JOURNAL Patent: US 5994095-A 23 30-NOV-1999;
FEATURES
source Location/Qualifiers
1..16 /organism="unknown"
/mol_type="unassigned DNA"

Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred.No.54;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Y 10 CGGTACAGGGAGTCC 25
|||||
b 1 CGGTGCCAGGAGCC 16

RESULT 46
LOCUS AR118047 16 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 23 from patent US 6140473.
ACCESSION AR118047
VERSION AR118047.1 GI:14098953
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kamb,A.
TITLE Antibodies specific for MTS2 Polypeptide
JOURNAL Patent: US 6140473-A 23 31-OCT-2000;
FEATURES
source Location/Qualifiers
1..16 /organism="unknown"
/mol_type="unassigned DNA"

Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred.No.54;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Y 10 CGGTACAGGGAGTCC 25
|||||
b 1 CGGTGCCAGGAGCC 16

RESULT 47
LOCUS AR127766 16 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 23 from patent US 6180776.
ACCESSION AR127766
VERSION AR127766.1 GI:14114361
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kamb,A.
TITLE MTS2 gene
JOURNAL Patent: US 6180776-A 23 30-JAN-2001;

FEATURES
source Location/Qualifiers
1..16 /organism="unknown"
/mol_type="unassigned DNA"

Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred.No.54;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Y 10 CGGTACAGGGAGTCC 25
|||||
b 1 CGGTGCCAGGAGCC 16

RESULT 48
LOCUS AR144933 16 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 23 from patent US 6210949.
ACCESSION AR144933
VERSION AR144933.1 GI:15106800
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Stone,S., Jiang,P. and Kamb,A.
TITLE Mouse MTS2 gene
JOURNAL Patent: US 6210949-A 23 03-APR-2001;
FEATURES
source Location/Qualifiers
1..16 /organism="unknown"
/mol_type="unassigned DNA"

Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred.No.54;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Y 10 CGGTACAGGGAGTCC 25
|||||
b 1 CGGTGCCAGGAGCC 16

RESULT 49
LOCUS AR145934 16 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 23 from patent US 6218146.
ACCESSION AR145934
VERSION AR145934.1 GI:15109123
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kamb,A.
TITLE MTS2 gene
JOURNAL Patent: US 6218146-A 23 17-APR-2001;
FEATURES
source Location/Qualifiers
1..16 /organism="unknown"
/mol_type="unassigned DNA"

Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred.No.54;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Y 10 CGGTACAGGGAGTCC 25
|||||
b 1 CGGTGCCAGGAGCC 16

RESULT 50
LOCUS I41167 16 bp DNA linear PAT 13-MAY-1997

```

FINITION      Sequence 23 from patent US 5624819.
CESSION       I41167
RSION         I41167.1 GI:2081757
WORDS         Unknown.
URCE          Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 16)
AUTHORS      Skolnick,M.H., Cannon-Albright,L.A. and Kamb,A.
TITLE        Germline mutations in the MTS gene
JOURNAL      Patent: US 5624819-A 23 29-APR-1997;
ATUES        Location/Qualifiers
            1..16
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 54;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

10 CGGTACAGGAGTCC 25
|||||
1 CGTGCCAGGAGGCC 16

SULT 51
259424
CUS          17 bp DNA linear PAT 17-JUL-2003
FINITION     Regulation of repressor genes using nucleic acid molecules.
CESSION      BD259424
RSION        BD259424.1 GI:33069194
WORDS        JP 2002541795-A/7217.
URCE         unidentified
ORGANISM      unidentified
REFERENCE     1 (bases 1 to 17)
AUTHORS      Blatt,L., Zwick,M., Pavco,P. and Meswiggen,J.
TITLE        Regulation of repressor genes using nucleic acid molecules
JOURNAL      Patent: JP 2002541795-A 7217 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT      OS Eukaryote
            PN JP 2002541795-A/7217
            PD 10-DEC-2002
            PF 11-APR-2000 JP 2000611654
            PR 12-APR-1999 US 60/129390
            PT LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
            C12R1:91),
            PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC A61K37/02,
            PC (C12N5/00,C12R1:91)
            CC Regulation of repressor genes using nucleic acid molecules FH
            Key source      1..17
            Location/Qualifiers
            FT source      /organism="Eukaryote".
            FT              Location/Qualifiers
            source        1..17
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 61;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

7 CTACGTACAGGAG 22
|||||
1 CTACATGTACAGGAG 16

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RESULT 52
AX265559/c
LOCUS         17 bp DNA linear PAT 26-OCT-2001
DEFINITION    Sequence 2950 from Patent WO0173002.
ACCESSION     AX265559
VERSION       AX265559.1 GI:16514358
KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Homo sapiens
REFERENCE     1
AUTHORS      Kmiec,E.B., Gamper,H.B. and Rice,M.C.
TITLE        Targeted chromosomal genomic alterations with modified single
            stranded oligonucleotides
JOURNAL      Patent: WO 0173002-A 2950 04-OCT-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES      Location/Qualifiers
            source        1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 61;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY          9 ACGTGTACAGGAGTC 24
DB          17 ACTGTCCAGGAGGC 2

RESULT 53
AX265560
LOCUS         17 bp DNA linear PAT 26-OCT-2001
DEFINITION    Sequence 2951 from Patent WO0173002.
ACCESSION     AX265560
VERSION       AX265560.1 GI:16514359
KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Homo sapiens
REFERENCE     1
AUTHORS      Kmiec,E.B., Gamper,H.B. and Rice,M.C.
TITLE        Targeted chromosomal genomic alterations with modified single
            stranded oligonucleotides
JOURNAL      Patent: WO 0173002-A 2951 04-OCT-2001;
            UNIVERSITY OF DELAWARE (US)
FEATURES      Location/Qualifiers
            source        1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 61;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY          9 ACGTGTACAGGAGTC 24
DB          1 ACTGTCCAGGAGGC 16

RESULT 54
AX688611
LOCUS         17 bp DNA linear PAT 31-MAR-2003
DEFINITION    Sequence 1343 from Patent EP1281758.
ACCESSION     AX688611
VERSION       AX688611.1 GI:29411313
KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 1343 05-FEB-2003;
Aemica, Inc. (US)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 61;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Y 10 CGTGTCAGGAGTCC 25
|||||
1 CGTGTCAGGAGTGC 16

RESULT 55
AX783827/c 17 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Sequence 2158 from Patent WO03050284.
ACCESSION AX783827
VERSION AX783827.1 GI:32951676
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Guo,J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 2158 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 61;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Y 13 GTACAGGAGTCCAGG 28
|||||
17 GAAAGGGAGTCAAGG 2

RESULT 56
AX783829/c 17 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Sequence 2160 from Patent WO03050284.
ACCESSION AX783829
VERSION AX783829.1 GI:32951678
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Guo,J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 2160 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source 1..17
/organism="Homo sapiens"

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 61;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Y 12 TGTACAGGAGTCCAG 27
|||||
16 TGAAGGGAGTCAAG 1

RESULT 57
AX783972/c 17 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Sequence 2303 from Patent WO03050284.
ACCESSION AX783972
VERSION AX783972.1 GI:32951821
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Guo,J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 2303 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 61;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Y 6 CCTACGTTACAGGGA 21
|||||
17 CCTACGTATAAGAGA 2

RESULT 58
AX783974/c 17 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Sequence 2305 from Patent WO03050284.
ACCESSION AX783974
VERSION AX783974.1 GI:32951823
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Guo,J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 2305 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 61;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Y 5 CCTACGTTACAGGG 20
|||||
16 CCTACGTATAAGAG 1

```

RESULT 59
LOCUS AR033355 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 121 from patent US 5869253.
ACCESSION AR033355
VERSION AR033355.1 GI:5948960
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting hepatitis C virus replication
JOURNAL Patent: US 5869253-A 121 09-FEB-1999;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 2 GGGCCCTACGTGTA 15
|||||
1 GGGCCCTCCGTGCA 14

RESULT 60
LOCUS AR113177 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 121 from patent US 6132966.
ACCESSION AR113177
VERSION AR113177.1 GI:14093499
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting hepatitis C virus replication
JOURNAL Patent: US 6132966-A 121 17-OCT-2000;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 2 GGGCCCTACGTGTA 15
|||||
1 GGGCCCTCCGTGCA 14

RESULT 61
LOCUS AR033355 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 121 from patent US 5610054.
ACCESSION AR033355
VERSION AR033355.1 GI:2482648
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Enzymatic RNA molecule targeted against Hepatitis C virus
JOURNAL Patent: US 5610054-A 121 11-MAR-1997;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 2 GGGCCCTACGTGTA 15
|||||
1 GGGCCCTCCGTGCA 14

/organism="unknown"
/mol_type="unassigned DNA"

Query Match 38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 2 GGGCCCTACGTGTA 15
|||||
1 GGGCCCTCCGTGCA 14

RESULT 62
LOCUS AR180569 15 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 637 from patent US 6333152.
ACCESSION AR180569
VERSION AR180569.1 GI:20222602
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
TITLE Gene expression profiles in normal and cancer cells
JOURNAL Patent: US 6333152-A 637 25-DEC-2001;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 5 ACAGGAGTCCAGG 28
|||||
14 ACAGAGAGTCCATG 1

RESULT 63
LOCUS BD207088 15 bp RNA linear PAT 17-JUL-2003
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
ACCESSION BD207088
VERSION BD207088.1 GI:33016858
KEYWORDS JP 2002512791-A/678.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 15)
AUTHORS Blatt,L., McSwiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 678 08-MAY-2002;
COMMENT RISOZYME PHARMACEUTICALS INC
OS Hepatitis virus (hepatitis C virus)
FN JP 2002512791-A/678
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
PAVCO,
PI DENNIS MACEJAK
PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
hepatitis C virus infection.
PH Key Location/Qualifiers


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FT source 1..15
FT /organism='Hepatitis virus (hepatitis C FT
virus)',
FEATURES
source
1..15
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"

Query Match 38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 2 GGGCCCTACGTGTA 15
| | | | |
b 1 GGGCCCTCCGTGCA 14

RESULT 64
ID065320/c
LOCUS BD065320 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Characterization of the yeast transcriptome.
ACCESSION BD065320
VERSION BD065320.1 GI:22610923
KEYWORDS JP 2001509017-A/256.
SOURCE Saccharomyces cerevisiae (baker's yeast)
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
1 (bases 1 to 10)
Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
Characterization of the yeast transcriptome
Patent: JP 2001509017-A 256 10-JUL-2001;
THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
OS Saccharomyces cerevisiae (yeast)
PN JP 2001509017-A/256
PD 10-JUL-2001
PF 22-JAN-1998 JP 1998532117
PR 23-JAN-1997 US 60/035917
PI VICTOR E VELCULESCU,BERT VOGELSTEIN,KENNETH W KINZLER PC
C12N15/10,C12N15/31,C07K14/395,C12Q1/68,C12Q1/02 CC
Characterization of the yeast transcriptome
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Saccharomyces cerevisiae (yeast)',
FEATURES
source
1..10
Location/Qualifiers
/organism="Saccharomyces cerevisiae"
/mol_type="genomic DNA"
/db_xref="taxon:4932"

Query Match 35.7%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 14 TACAGGGAGT 23
| | | | |
b 10 TACAGGGAGT 1

RESULT 65
X470525/c
LOCUS AX470525 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 102 from Patent WO2053773.
ACCESSION AX470525
VERSION AX470525.1 GI:22205650
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Hofmann,K., Conradt,M. and Petersohn,D.
REFERENCE
AUTHORS

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TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 102 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 35.7%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 12 TGTACAGGGA 21
| | | | |
b 10 TGTACAGGGA 1

RESULT 66
AX629206/c
LOCUS AX629206 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6247 from Patent WO02053774.
ACCESSION AX629206
VERSION AX629206.1 GI:28457244
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 6247 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
JOURNAL
FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 35.7%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 12 TGTACAGGGA 21
| | | | |
b 10 TGTACAGGGA 1

RESULT 67
AR033531
LOCUS AR033531 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 297 from patent US 5869253.
ACCESSION AR033531
VERSION AR033531.1 GI:5949136
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting hepatitis C virus replication
JOURNAL Patent: US 5869253-A 297 09-FEB-1999;
FEATURES
source
1..15
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 35.7%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 19 GGAGTCCAGG 28

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|||||
3 GGAGTCCAGG 12

RESULT 68
LOCUS AR113353 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 297 from patent US 6132966.
ACCESSION AR113353
KEYWORDS AR113353.1 GI:14093675
SOURCE Unknown.
ORIGIN Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper K.G.
TITLE Method and reagent for inhibiting hepatitis C virus replication
JOURNAL Patent: US 6132966-A 297 17-OCT-2000;
FEATURES Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 35.7%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
19 GGAGTCCAGG 28
|||||
3 GGAGTCCAGG 12

RESULT 69
LOCUS I38986 15 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 24 from patent US 5616488.
ACCESSION I38986
KEYWORDS I38986.1 GI:2083466
SOURCE Unknown.
ORIGIN Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Sullivan, S., Draper, K.G., McSwiggen, J., and Stinchcomb, D.T.
TITLE IL-5 targeted ribozymes
JOURNAL Patent: US 5616488-A 24 01-APR-1997;
FEATURES Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 35.7%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
6 CCTACGTGTA 15
|||||
5 CCTACGTGTA 14

RESULT 70
LOCUS I57760 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 297 from patent US 5610054.
ACCESSION I57760
KEYWORDS I57760.1 GI:2482824
SOURCE Unknown.
ORIGIN Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper K.G.
TITLE Enzymatic RNA molecule targeted against Hepatitis C virus

JOURNAL Patent: US 5610054-A 297 11-MAR-1997;
FEATURES Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 35.7%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
19 GGAGTCCAGG 28
|||||
3 GGAGTCCAGG 12

RESULT 71
LOCUS AX635280 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 2419 from Patent EP1260586.
ACCESSION AX635280
KEYWORDS AX635280.1 GI:28470894
SOURCE unidentified
ORIGIN unidentified
REFERENCE 1
AUTHORS Stinchcomb, D.T., Dudycz, L.W., Chowrira, B., Grimm, S., Drenzo, A., Karpel, A., Draper, K.G., Kisch, K., Matulic-Adamic, J., McSwiggen, J.A., Modak, A., Pavco, P., Beigelman, L., Sullivan, S.M., Sweedler, D., Thompson, J.D., Tracz, D., Ueman, N., Wincott, F.E. and Woolf, T.
TITLE Method and reagent for inhibiting the expression of disease related genes

JOURNAL Patent: EP 1260586-A 2419 27-NOV-2002;
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers
1..15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match 35.7%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
6 CCTACGTGTA 15
|||||
5 CCTACGTGTA 14

RESULT 72
LOCUS BD207264 15 bp RNA linear PAT 17-JUL-2003
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
ACCESSION BD207264.1 GI:33017034
KEYWORDS JP 2002512791-A/854.
SOURCE unidentified
ORIGIN unidentified

REFERENCE 1 (bases 1 to 15)
AUTHORS Blatt, J., McSwiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 854 08-MAY-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/854
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 6C/083217, 18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608, 23-MAR-1999 US 09/274553 PI

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LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI
PI DENNIS MACEJAK
PC C12N9/00, A61K31/7105, A61K38/21, A61K48/00, A61P31/12, C12N15/09,
PC A61K37/66,
PC C12N15/00,
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
CC hepatitis C virus infection.
FH Key Location/Qualifiers
FT source 1..15
FT virus),
FT Location/Qualifiers
FT 1..15
/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"

Query Match 35.7%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 19 GGAGTCCAGG 28
|||||
b 3 GGAGTCCAGG 12

RESULT 73
LOCUS A42545 14 bp DNA linear PAT 06-MAR-1997
DEFINITION Sequence 61 from Patent WO9502051.
ACCESSION A42545
VERSION A42545.1 GI:2297994
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen, G., Schlingensiepen, R., Schlingensiepen, K. and Brysch, W.
TITLE A PHARMACEUTICAL COMPOSITION COMPRISING ANTISENSE-NUCLEIC ACID FOR PREVENTION AND/OR TREATMENT OF NEURONAL INJURY, DEGENERATION AND CELL DEATH AND FOR THE TREATMENT OF NEOPLASMS
JOURNAL Patent: WO 9502051-A 61 19-JAN-1995; BIOGNOSTIK GES FUER BIOMOLEKUL (DE)
COMMENT Other publication AU 7345694 950206.
FEATURES
source 1..14
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 35.0%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 85;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

y 10 CGGTACAGGAG 22
|||||
b 2 CGGTACAGGAG 14

RESULT 74
LOCUS A88736 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 884 from Patent WO9833904.
ACCESSION A88736
VERSION A88736.1 GI:6737306
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 14)

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Brysch, W. and Schlingensiepen, K.
AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
PATENT: WO 9833904-A 884 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source 1..14
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 35.0%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 85;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

y 10 CGGTACAGGAG 22
|||||
b 2 CGGTACAGGAG 14

RESULT 75
LOCUS AR253087/c 14 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 38 from patent US 6479242.
ACCESSION AR253087
VERSION AR253087.1 GI:27301448
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Guo, B. and Sun, X.
TITLE Method for genotyping of single nucleotide polymorphism
JOURNAL Patent: US 6479242-A 38 12-NOV-2002;
FEATURES
source 1..14
/organism="unknown"
/mol_type="genomic DNA"

Query Match 35.0%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 85;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

y 12 TGTACAGGAGTC 24
|||||
b 14 TGGCAGGAGTC 2

RESULT 76
LOCUS BD066249 14 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066249
VERSION BD066249.1 GI:22611852
KEYWORDS JP 2001511000-A/884.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen, K. H. and Brysch, W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 884 07-AUG-2001; BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT
OS Unknown
PN JP 2001511000-A/884
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
PC C12N15/11, C07H21/04, A61K31/70
CC An antisense oligonucleotide preparation method FH Key
SOURCE Location/Qualifiers
FT source 1..14
/organism="Unknown".

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FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32644"

Query Match
Best Local Similarity 35.0%; Score 9.8; DB 1; Length 14;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

10 CGTCTACAGGAG 22
2 CGTCTAGAGAG 14

RESULT 77
LOCUS             15 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION       Adeno-associated virus-delivered ribozyme compositions and methods
ACCESSION       AR033349
VERSION         Sequence 115 from patent US 5862953.
KEYWORDS        AR033349
SOURCE          AR033349.1 GI:5948954
ORGANISM        Unknown.
REFERENCE       1 (bases 1 to 15)
AUTHORS        Draper,K.G.
TITLE          Method and reagent for inhibiting hepatitis C virus replication
JOURNAL        Patent: US 5862953-A 115 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1..15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Query Match
Best Local Similarity 35.0%; Score 9.8; DB 1; Length 15;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

3 GGCCCTACGTGTA 15
2 GGCCCTACGTATA 14

RESULT 78
LOCUS             15 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION       Adeno-associated virus-delivered ribozyme compositions and methods
ACCESSION       AR113171
VERSION         Sequence 115 from patent US 6132966.
KEYWORDS        AR113171
SOURCE          AR113171.1 GI:14093493
ORGANISM        Unknown.
REFERENCE       1 (bases 1 to 15)
AUTHORS        Draper,K.G.
TITLE          Method and reagent for inhibiting hepatitis C virus replication
JOURNAL        Patent: US 6132966-A 115 17-OCT-2000;
FEATURES             Location/Qualifiers
     source          1..15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Query Match
Best Local Similarity 35.0%; Score 9.8; DB 1; Length 15;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

3 GGCCCTACGTGTA 15
2 GGCCCTACGTATA 14

RESULT 79
LOCUS             15 bp      RNA      linear      PAT 17-JUL-2003
DEFINITION       Adeno-associated virus-delivered ribozyme compositions and methods
ACCESSION       BD263790
VERSION         BD263790.1 GI:33073558
KEYWORDS        JP 2002542805-A/12.
SOURCE          JP 2002542805-A/12.
ORGANISM        synthetic construct
                synthetic construct
                artificial sequences.
REFERENCE       1 (bases 1 to 15)
AUTHORS        Lewin,A.S., Muzyczka,N., Hauswirth,W.W., Teschendorf,C. and
                Burger,C.
TITLE          Adeno-associated virus-delivered ribozyme compositions and methods
                of use
JOURNAL        Patent: JP 2002542805-A 12 17-DEC-2002;
                UNIVERSITY OF FLORIDA
COMMENT        OS Artificial Sequence
                PN JP 2002542805-A/12
                PD 17-DEC-2002
                PF 28-APR-2000 JP 2000615402
                PR 30-APR-1999 US 60/131942
                PI ALFRED S LEWIN,NICHOLAS MUZYCZKA,WILLIAM W HAUSWIRTH PI
                ,CHRISTIAN TESCHENDORF,
                PI CORINNA BURGER
                PC C12N15/09,A01K67/027,C12N9/00,C12Q1/68,C12N15/00 CC
                Description of Artificial Sequence: SYNTHETIC PEPTIDE PH Key
                Location/Qualifiers
                FT source 1..15
                FT Location/Qualifiers
                 source 1..15
                  Location/Qualifiers
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                   /db_xref="taxon:32630"

Query Match
Best Local Similarity 35.0%; Score 9.8; DB 1; Length 15;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

16 CAGGAGTCCAGG 28
1 CAGACAGTCCAGG 13

RESULT 80
LOCUS             15 bp      DNA      linear      PAT 07-OCT-1997
DEFINITION       Adeno-associated virus-delivered ribozyme compositions and methods
ACCESSION       I57578
VERSION         Sequence 115 from patent US 5610054.
KEYWORDS        I57578
SOURCE          I57578.1 GI:2482642
ORGANISM        Unknown.
REFERENCE       1 (bases 1 to 15)
AUTHORS        Draper,K.G.
TITLE          Enzymatic RNA molecule targeted against Hepatitis C virus
JOURNAL        Patent: US 5610054-A 115 11-MAR-1997;
FEATURES             Location/Qualifiers
     source          1..15
                     /organism="unknown"
                     /mol_type="unassigned DNA"

Query Match
Best Local Similarity 35.0%; Score 9.8; DB 1; Length 15;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

3 GGCCCTACGTGTA 15
2 GGCCCTACGTATA 14

RESULT 81

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X048276
ACCU Sequence 12 from Patent WO0066780. linear PAT 15-DEC-2000
CCESION AX048276 15 bp RNA
ERSON AX048276.1 GI:11877041
EYWORDS synthetic construct
ORGANISM synthetic construct
SOURCE artificial sequences.
REFERENCE
1 Lewin,A.S., Muzyczka,N., Hauswirth,W.W., Teschendorf,C. and
AUTHORS Burger,C.
TITLE Adeno-associated virus-delivered ribozyme compositions and methods
of use
JOURNAL Patent: WO 0066780-A 12 09-NOV-2000;
UNIVERSITY of Florida (US)
FEATURES
source
1. .15
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32830"
/notes="SYNTHETIC PEPTIDE"
Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 97;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
y 16 CAGGAGTCCAGG 28
| | | | |
b 1 CAGACAGTCCAGG 13

RESULT 82
X362585/c
ACCU Sequence 19 from Patent WO0208425. linear PAT 15-FEB-2002
CCESION AX362585 15 bp DNA
ERSON AX362585
EYWORDS AX362585.1 GI:18694729
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Finkel,K. and Koshy,B.
AUTHORS Haplotypes of the adrb3 gene
TITLE Patent: WO 0208425-A 19 31-JAN-2002;
JOURNAL Genaisance Pharmaceuticals, Inc. (US)
FEATURES
source
1. .15
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 97;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
y 11 GTGTACAGGGAGT 23
| | | | |
b 13 GTGCCAGGGAGT 1

RESULT 83
ID207082
ACCU Enzymatic nucleic acid treatment of diseases or conditions related
REFERENCE to hepatitis C virus infection. linear PAT 17-JUL-2003
CCESION BD207082 15 bp RNA
ERSON BD207082.1 GI:33016852
EYWORDS JP 2002512791-A/672.
ORGANISM unidentified
unidentified

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unclassified.
1 (bases 1 to 15)
REFERENCE
AUTHORS Blatt,L., McSwiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 672 08-MAY-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/672
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI
PAVCO,
PI DENNIS MACEJAK
PC C12N9/00,A61K31/7105,A61K48/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
CC hepatitis C virus infection.
FH Key Location/Qualifiers
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/organism="Hepatitis virus (hepatitis C FT
virus)",
Location/Qualifiers
1. .15
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/mol_type="genomic RNA"
/db_xref="taxon:32644"
Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 97;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
y 3 GCCCTACGTGTA 15
| | | | |
b 2 GCCCTACGTATA 14

RESULT 84
AX625951/c
LOCUS AX625951 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2992 from Patent WO02053774.
ACCESSION AX625951
VERSION AX625951.1 GI:28453989
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 2992 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 33.6%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
y 12 TGTACAGGGAG 22
| | | | |
b 11 TGTACAGGGAG 1

RESULT 85

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627912/c
ACUS AX627912 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4953 from Patent WO02053774.
JOURNAL
FEATURES
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4953 11-JUL-2002; (DE)
FEATURES
SOURCE Location/Qualifiers
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Query Match 33.6%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
18 GGGAGTCCAGG 28
|||||
11 GGGATCCAGG 1
RESULT 86
628430/c
ACUS AX628430 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5471 from Patent WO02053774.
JOURNAL
FEATURES
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5471 11-JUL-2002; (DE)
FEATURES
SOURCE Location/Qualifiers
1.11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 33.6%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
18 GGGAGTCCAGG 28
|||||
11 GGGATCCAGG 1
RESULT 87
628528/c
ACUS AX628528 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5569 from Patent WO02053774.
JOURNAL
FEATURES
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE

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AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5569 11-JUL-2002; (DE)
FEATURES
SOURCE Location/Qualifiers
1.11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 33.6%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 12 TGTACAGGAG 22
|||||
Db 11 TGTACAGGAG 1
RESULT 88
AR199211
LOCUS AR199211 12 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 67 from patent US 6355423.
ACCESSION AR199211
VERSION AR199211.1 GI:20249285
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 12)
Rothberg,J.Warc., Nallur,G.N. and Hu,X.
TITLE Methods and devices for measuring differential gene expression
JOURNAL Patent: US 6355423-A 67 12-MAR-2002;
FEATURES
SOURCE Location/Qualifiers
1.12
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 33.6%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 76;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 6 CCTACGCTGATC 16
|||||
Db 2 CCTACGCTGATC 12
RESULT 89
AR362486
LOCUS AR362486 12 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 2 from patent US 5174962.
ACCESSION AR362486
VERSION AR362486.1 GI:34422687
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 12)
Brennan,T.W.
TITLE Apparatus for determining DNA sequences by mass spectrometry
JOURNAL Patent: US 5174962-A 2 29-DEC-1992;
FEATURES
SOURCE Location/Qualifiers
1.12
/organism="unknown"
/mol_type="genomic DNA"
Query Match 33.6%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 76;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 9 ACGGTGATCAGG 19
|||||
Db 1 ACGGTGATCAGG 11

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14 CGTGATCAGGCGT 1					
SULT 95	AX711052	linear	PAT 11-APR-2003		
CUS	Sequence 352 from Patent EP1288296.	14 bp RNA			
FINITION	SESSION	AX711052			
RSION	AX711052.1	GI:29787433			
WORDS					
ORGANISM	Herpes simplex virus unknown type				
	Herpes simplex virus unknown type				
	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;				
	Alphaherpesvirinae; Simplexvirus.				
REFERENCE					
AUTHORS	Draper,K.G., McSwigen,J.A., Holecsek,J.J., Dudycz,L.W.,				
	Macejak,D.G. and Mamone,A.J.				
TITLE	Method and reagent for inhibiting HBV viral replication				
JOURNAL	PATENT: JP 1288296-A 352 05-MAR-2003;				
	RIBOZYME PHARMACEUTICALS, INC. (US)				
ATURES	Location/Qualifiers				
source	1..14				
	/organism="Herpes simplex virus unknown type"				
	/mol_type="unassigned RNA"				
	/db_xref="taxon:126283"				
Query Match	32.9%; Score 9.2; DB 1; Length 14;				
Best Local Similarity	78.6%; Pred. No. 1.2e+02;				
Matches	11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
	10 CGGTACAGGCGT 23				
	14 CGTGATCAGGCGT 1				
SULT 96	BD001174	linear	PAT 31-JAN-2002		
CUS	Method and reagent for inhibiting viral replication.	14 bp RNA			
FINITION	BD001174				
SSION	BD001174.1	GI:18625733			
RSION	JP 2000342285-A/334.				
WORDS	synthetic construct				
ORGANISM	artificial sequences.				
	1 (bases 1 to 14)				
REFERENCE	Draper,K.G., Dadyktz,L.W., Macswigen,J.A., Maysejak,D.G.,				
AUTHORS	Holecsek,J.J. and Mamone,A.J.				
TITLE	Method and reagent for inhibiting viral replication				
JOURNAL	PATENT: JP 2000342285-A 334 12-DEC-2000;				
	RIBOZYME PHARMACEUTICALS INC				
COMMENT	OS Artificial Sequence				
	PN JP 2000342285-A/334				
	PD 12-DEC-2000				
	PF 01-MAY-2000 JP 2000132616				
	PR 11-MAY-1992 US 07/882689,14-MAY-1992 US 07/882712 PR				
	14-MAY-1992 US 07/882713,14-MAY-1992 US 07/882714 PR				
	14-MAY-1992 US 07/882823,14-MAY-1992 US 07/882824 PR				
	14-MAY-1992 US 07/882886,14-MAY-1992 US 07/882888 PR				
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	14-MAY-1992 US 07/882922,14-MAY-1992 US 07/883823 PR				
	14-MAY-1992 US 07/883849,14-MAY-1992 US 07/884073 PR				
	14-MAY-1992 US 07/884074,14-MAY-1992 US 07/884333 PR				
	14-MAY-1992 US 07/884422,14-MAY-1992 US 07/884431 PR				
	14-MAY-1992 US 07/884436,14-MAY-1992 US 07/884521 PR				
	31-JUL-1992 US 07/923738,26-AUG-1992 US 07/935854 PR				
	26-AUG-1992 US 07/936086,18-SEP-1992 US 07/948359 PR				
	15-OCT-1992 US 07/963322,07-DEC-1992 US 07/987129 PR				
	KENNETH G DRAPER,LEC W DADYKTZ,JAMES A MACSWIGEN, PI DENNIS G				
	MAYSEJAK,				
	PI JAMES J HOLESEK ANTHONY J MAMONE				
	PC C12N15/09,C12N5/10,C12N7/00//A61K38/43,A61K39/125,A61K39/13,				
	PC A61K39/135,A61K39/21,A61K39/23,A61K39/245,A61K39/29,A61K48/00,				
	PC A61P1/16,				
	PC A61P3/14,A61P3/16,A61P3/18,A61P31/22,A61P35/02,C12Q1/68,PC				
	(C12N15/09,C12R1:93),C12N15/00,C12N5/00,A61K37/48,(C12N15/00,PC				
	C12R1:93)				
	CC Key Location/Qualifiers				
FH	1..14				
FT	source /organism='Artificial Sequence'				
FEATURES	1..14				
source	/organism="synthetic construct"				

/mol_type="genomic RNA"
/db_xref="taxon:32630"

Query Match 32.9%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Y 10 CGTGTACGGGACT 23
| | | | |
b 14 CGTGATCAGGGCGT 1

RESULT 98
LOCUS BD066348 14 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066348
VERSION BD066348.1 GI:22611951
KEYWORDS JP 2001511000-A/983.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiefen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 983 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/983
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEFEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
FT source 1..14
FT Location/Qualifiers
1..14
/organism='Unknown'.

FEATURES
source
1..14
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 32.9%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Y 6 CCTACGTGTACAGG 19
| | | | |
b 14 CCTCTGTATACAGG 1

RESULT 99
LOCUS AX152114 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 29 from Patent WO0138577.
ACCESSION AX152114
VERSION AX152114.1 GI:14533765
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcripomes
JOURNAL Patent: WO 0138577-A 29 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
1..10
/organism="Homo sapiens"
/mol_type="unassigned DNA"

FEATURES
source
1..10

/db_xref="taxon:9606"

Query Match 32.1%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 GAGTCCAGG 28
| | | | |
Db 2 GAGTCCAGG 10

RESULT 100
LOCUS AX626581 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3622 from Patent WO02053774.
ACCESSION AX626581
VERSION AX626581.1 GI:28454619
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3622 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 32.1%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGAGTCCAG 27
| | | | |
Db 9 GGAGTCCAG 1

RESULT 101
LOCUS AX628461 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5502 from Patent WO02053774.
ACCESSION AX628461
VERSION AX628461.1 GI:28456499
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5502 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

source

Query Match 32.1%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TAGCTGTAC 16
| | | | |
Db 11 TAGCTGTAC 3

Y 13 GTACAGGAGTC 24
 |||||
 b 12 GTACAGTAGGC 1

RESULT 106

97287
 OCUS A97287 12 bp DNA linear PAT 26-JAN-2000
 DEFINITION Sequence 4 from Patent WO9918197.
 CESSION A97287
 ERSION A97287.1 GI:6780670
 EYWORDS
 SOURCE

ORGANISM

unidentified
 unclassified

REFERENCE 1 (bases 1 to 12)

AUTHORS Yaspo,M. and Lehrach,H.
 TITLE NUCLEIC ACID MOLECULE ENCODING A (POLY)PEPTIDE CO-SEGREGATING IN
 MUTATED FORM WITH AUTOIMMUNE POLYENDOCRINOPATHY CANDIDIASIS
 ECTODERMAL DYSTROPHY (APECED)

JOURNAL Patent: WO 9918197-A 4 15-APR-1999;

MAX PLANCK GESLLSCHAFT (DE); YASPO MARIE LAURE (DE)

FEATURES

source
 1..12
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"

Query Match

Best Local Similarity 31.4%; Score 8.8; DB 1; Length 12;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 15 ACAGGGAGTGCCA 26
 |||||
 b 1 ACAGGCAGGCCA 12

RESULT 107

R167847/c
 OCUS AR167847 12 bp DNA linear PAT 17-DEC-2001
 DEFINITION Sequence 211 from patent US 6287769.
 CESSION AR167847
 ERSION AR167847.1 GI:17903654

KEYWORDS

Unknown.

ORGANISM

unclassified.

REFERENCE 1 (bases 1 to 12)

AUTHORS Inoue,T.
 TITLE Method of amplifying DNA fragment, apparatus for amplifying DNA
 fragment, method of assaying microorganisms, method of analyzing
 microorganisms and method of assaying contaminant

JOURNAL Patent: US 6287769-A 211 11-SEP-2001;

FEATURES

source
 1..12
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match

Best Local Similarity 31.4%; Score 8.8; DB 1; Length 12;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 5 CCTACCGTGTCAC 16
 |||||
 b 12 CCATACGTGCAC 1

RESULT 108

129731/c
 OCUS E29731 12 bp DNA linear PAT 18-JUN-2001
 DEFINITION Method for amplifying DNA fragment, method for estimating state of
 microorganism existing and method for estimating state of waste.

ACCESSION

E29731

VERSION E29731.1 GI:13021234
 KEYWORDS JP 1999276176-A/211.
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.

REFERENCE 1 (bases 1 to 12)

AUTHORS Koichi, I.

TITLE Method for amplifying DNA fragment, method for estimating state of
 microorganism existing and method for estimating state of waste

JOURNAL Patent: JP 1999276176-A 211 12-OCT-1999;

SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE

FORESTRY AND FISHERIES

COMMENT OS Unidentified

PN JP 1999276176-A/211

PD 12-OCT-1999

PF 31-MAR-1998 JP 1998087652

PR KOICHI INOUE

PC C12N15/09,B09B3/00,C12Q1/00,C12Q1/68,C12N15/00,B09B3/00 CC

Strandedness: Single;

FH Key Location/Qualifiers

FT source 1..12 /organism='Unidentified'.

FEATURES Location/Qualifiers

source
 1..12
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

Query Match 31.4%; Score 8.8; DB 1; Length 12;

Best Local Similarity 83.3%; Pred. No. 1e+02;

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCCTACGTGTAC 16
 |||||
 Db 12 CCATACGTGCAC 1

RESULT 109

E38837/c
 LOCUS E38837 12 bp DNA linear PAT 31-JAN-2002
 DEFINITION Method and device for amplifying DNA fragment.
 E38837

ACCESSION E38837

VERSION E38837.1 GI:18621499

KEYWORDS JP 2000270867-A/211.

SOURCE unidentified

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 12)

AUTHORS Inoue,K.

TITLE Method and device for amplifying DNA fragment

JOURNAL Patent: JP 2000270867-A 211 03-OCT-2000;

SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE

FORESTRY AND FISHERIES

COMMENT OS Unidentified

PN JP 2000270867-A/211

PD 03-OCT-2000

PF 19-MAR-1999 JP 1999076844

PR KOICHI INOUE

PC C12N15/09,C12M1/00,C12Q1/68,C12N15/00

Strandedness: Single;

CC Topology: Linear;

FH Key Location/Qualifiers

FT source 1..12 /organism='Unidentified'.

FEATURES Location/Qualifiers

source
 1..12
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

Query Match

31.4%; Score 8.8; DB 1; Length 12;

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Best Local Similarity 83.3%; Pred. No. 1e+02; Mismatches 0; Indels 2; Gaps 0;
Matches 10; Conservative 0;

/
5 CCTACGTGTAC 16
|||
12 CCATACGTGCAC 1

RESULT 110
LOCUS 4263/c
DEFINITION 12 bp DNA linear PAT 18-JUN-2001
METHOD for amplifying DNA fragment, amplification apparatus of DNA
fragment, method for assaying a group of microorganisms, method
for analyzing a group of microorganisms, and method for assaying
contaminating substance.
ACCESSION E64263
KEYWORDS E64263.1 GI:13019667
SOURCE JP 1999341989-A/211.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 12)
AUTHORS Koichi, I.
TITLE Method for amplifying DNA fragment, amplification apparatus of DNA
fragment, method for assaying a group of microorganisms, method for
analyzing a group of microorganisms, and method for assaying
contaminating substance
JOURNAL Patent: JP 1999341989-A 211 14-DEC-1999;
SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
FORESTRY AND FISHERIES
COMMENT OS Artificial Sequence
PN JP 1999341989-A/211
PD 14-DEC-1999
PF 16-MAR-1999 JP 1999069694
PR KOICHI INOUE
PI C12N15/09,C12M1/00,C12Q1/68,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..12
FEATURES
source Location/Qualifiers
1..12
/mol_type="synthetic construct"
/db_xref="taxon:32630"

Query Match 31.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

/
5 CCTACGTGTAC 16
|||
12 CCATACGTGCAC 1

RESULT 111
LOCUS 407937
DEFINITION 13 bp RNA linear PAT 18-DEC-2003
SEQUENCE 30 from patent US 6632057.
ACCESSION AR407937
KEYWORDS AR407937.1 GI:40157924
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Fauchet,C.R.J
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 30 14-OCT-2003;
FEATURES
source Location/Qualifiers
1..13
/mol_type="unknown"

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/mol_type="unassigned RNA"

Query Match 31.4%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGGCGCCTACGT 12
|||
DB 1 CAGGCTCTACGT 12

RESULT 112
LOCUS AR088591/c
DEFINITION Sequence 7 from patent US 5989906.
ACCESSION AR088591
VERSION AR088591.1 GI:10015355
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Thompson,J.D.
TITLE Method and reagent for inhibiting P-glycoprotein (mdr-1-gene)
JOURNAL Patent: US 5989906-A 7 23-NOV-1999;
FEATURES
source Location/Qualifiers
1..10
/mol_type="unknown"

Query Match 30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 GGGAGTCCAG 27
|||
DB 10 GGAAGTCCAG 1

RESULT 113
LOCUS AR099558/c
DEFINITION Sequence 85 from patent US 6077833.
ACCESSION AR099558
VERSION AR099558.1 GI:12809324
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Bennett,C.Frank, and Vickers,T.A.
TITLE Oligonucleotide compositions and methods for the modulation of the
expression of B7 protein.
JOURNAL Patent: US 6077833-A 85 20-JUN-2000;
FEATURES
source Location/Qualifiers
1..10
/mol_type="unknown"

Query Match 30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 GTACAGGGAG 22
|||
DB 10 GTACGGGGAG 1

RESULT 114
LOCUS AR178839/c
DEFINITION Sequence 85 from patent US 6319906.
ACCESSION AR178839

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ERSION AR178839.1 GI:20219977
EYWORDS
ORCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Bennett,C.Frank, and Vickers,T.A.
TITLE Oligonucleotide compositions and methods for the modulation of the
JOURNAL expression of B7 protein
PATENT: US 6319905-A 85 20-NOV-2001;
FEATURES
source
Location/Qualifiers
1..10
/mol_type="unknown"
/mol_type="unassigned DNA"
Query Match 30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 13 GTACAGGGAG 22
b 10 GTACAGGGAG 1

RESULT 115
54652/c
LOCUS Human normal liver cell expression genes.
DEFINITION E54652
CESSION E54652
EYWORDS E54652.1 GI:22556135
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human normal liver cell expression genes
JOURNAL Patent: JP 2001211883-A 4 07-AUG-2001;
SCIENCE & TECH AGENCY
COMMENT OS Homo sapiens (human)
PN JP 2001211883-A/4
PD 07-AUG-2001
PF 31-JAN-2000 JP 2000023170
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K16/18,C12P21/02,C12N15/00
FH Key Location/Qualifiers.
FEATURES
source
1..10
/mol_type="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 18 GGGAGTCCAG 27
b 10 GGGAGGCCAG 1

RESULT 116
R336839
LOCUS Sequence 14 from patent US 6566130.
DEFINITION AR336839
CESSION AR336839
EYWORDS AR336839.1 GI:33722689
ORGANISM Unknown.
SOURCE Unknown.

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Unclassified.
1 (bases 1 to 10)
AUTHORS Srivastava,S., Moul,J.W., Xu,L.L. and Segawa,T.
TITLE Androgen-regulated Gene expressed in prostate tissue
JOURNAL Patent: US 6566130-A 14 20-MAY-2003;
FEATURES
source
Location/Qualifiers
1..10
/mol_type="genomic DNA"
/mol_type="unknown"
Query Match 30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 13 GTACAGGGAG 22
b 1 GTGACAGGGAG 10

RESULT 117
AX113024/c
LOCUS Sequence 71 from Patent WO0127267.
DEFINITION AX113024
CESSION AX113024
EYWORDS AX113024.1 GI:13939459
KEYWORDS Mus sp.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
AUTHORS Adams,E., Waldmann,H., Cobbold,S. and Zelenika,D.
TITLE Genes differentially expressed in trl cells and their use in the
JOURNAL manufacture of immunoregulatory compositions
PATENT: WO 0127267-A 71 19-APR-2001;
ISIS INNOVATION LIMITED (GB)
FEATURES
source
Location/Qualifiers
1..10
/mol_type="Mus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:10095"
Query Match 30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 12 TGTACAGGGA 21
b 10 TGTACGGGGA 1

RESULT 118
AX153342/c
LOCUS Sequence 1257 from Patent WO0138577.
DEFINITION AX153342
CESSION AX153342
EYWORDS AX153342.1 GI:14534993
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcripts
JOURNAL Patent: WO 0138577-A 1257 31-MAY-2001;
FEATURES
source
Location/Qualifiers
1..10
/mol_type="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Query Match      30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

12 TGTACAGGGA 21
|||||
10 TGTACGGGGA 1

RESULT 119
LOCUS AX377356 10 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 20 from Patent WO212499.
ACCESSION AX377356
VERSION AX377356.1 GI:19573642
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL Klem,S.E., Koshy,B. and Lanz,E.M.
COMMENT Haplotypes of the ntf3 gene
Patent: WO 0212499-A 20 14-FEB-2002;
Genaisance Pharmaceuticals, Inc. (US)
Location/Qualifiers
1..10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 CGGGCCCTAC 10
|||||
1 CGGGCCCTCC 10

RESULT 120
LOCUS BD166783 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166783
VERSION BD166783.1 GI:27872595
KEYWORDS JP 2002209591-A/328.
ORGANISM unidentified
SOURCE unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 328 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/328
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1..10
/organism="Homo sapiens (human)"
/mol_type="unidentified"
/db_xref="taxon:32644"

Query Match      30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 CGGGCCCTCC 10
|||||
1 CGGGCCCTCC 1

RESULT 121
LOCUS BD167020 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD167020
VERSION BD167020.1 GI:27872832
KEYWORDS JP 2002209591-A/565.
ORGANISM unidentified
SOURCE unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 565 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/565
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1..10
/organism="Homo sapiens (human)"
/mol_type="unidentified"
/db_xref="taxon:32644"

Query Match      30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

17 AGGAGTCCA 26
|||||
10 AGGGCGTCCA 1

RESULT 122
LOCUS BD167059 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD167059
VERSION BD167059.1 GI:27872871
KEYWORDS JP 2002209591-A/604.
ORGANISM unidentified
SOURCE unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 604 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/604
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI

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YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00,
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1..10
   /organism='Homo sapiens (human)'.
   Location/Qualifiers
   source 1..10
   /organism='unidentified'
   /mol_type='genomic DNA'
   /db_xref='taxon:32644'

Query Match 30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 18 GGGAGTCCAG 27
   |||||
Db 10 GGGAGGCCAG 1

RESULT 123
LOCUS BD167158 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD167158
VERSION BD167158.1 GI:27872970
KEYWORDS JP 200209591-A/703.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 200209591-A 703 30-JUL-2002;
JOURNAL JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 200209591-A/703
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00,
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
FT source 1..10
   /organism='Homo sapiens (human)'.
   Location/Qualifiers
   source 1..10
   /organism='unidentified'
   /mol_type='genomic DNA'
   /db_xref='taxon:32644'

Query Match 30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 89;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 18 GGGAGTCCAG 27
   |||||
Db 10 GGGAGGCCAG 1

RESULT 124
LOCUS AR099559 11 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 86 from patent US 6077833.
ACCESSION AR099559
VERSION AR099559.1 GI:12809325
KEYWORDS

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SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Bennett,C.Frank. and Vickers,T.A.
TITLE Oligonucleotide compositions and methods for the modulation of the
expression of B7 protein
JOURNAL Patent: US 6077833-A 86 20-JUN-2000;
FEATURES Location/Qualifiers
   source 1..11
   /organism='unknown'
   /mol_type='unassigned DNA'

Query Match 30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 13 GTACAGGGAG 22
   |||||
Db 11 GTACGGGGAG 2

RESULT 125
LOCUS AR178840 11 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 86 from patent US 6319906.
ACCESSION AR178840
VERSION AR178840.1 GI:20219978
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Bennett,C.Frank. and Vickers,T.A.
TITLE Oligonucleotide compositions and methods for the modulation of the
expression of B7 protein
JOURNAL Patent: US 6319906-A 86 20-NOV-2001;
FEATURES Location/Qualifiers
   source 1..11
   /organism='unknown'
   /mol_type='unassigned DNA'

Query Match 30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 13 GTACAGGGAG 22
   |||||
Db 11 GTACGGGGAG 2

RESULT 126
LOCUS BD241058 11 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods and products related to genotyping and DNA analysis.
ACCESSION BD241058
VERSION BD241058.1 GI:33050828
KEYWORDS JP 2002525127-A/5.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 11)
AUTHORS Landers,J.E., Jordan,B., Housman,D.E. and Charest,A.
TITLE Methods and products related to genotyping and DNA analysis
JOURNAL Patent: JP 2002525127-A 5 13-AUG-2002;
COMMENT OS Homo sapiens (human)
PN JP 2002525127-A/5
PD 13-AUG-2002
PF 24-SEP-1999 JP 2000572407
PR 25-SEP-1998 US 60/101757
PI JOHN E LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST PC

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C12N15/09, C12Q1/68, G01N33/53, G01N33/566, G01N33/58, G01N37/00, PC
 G01N37/00,
 PC C12N15/00
 CC Methods and products related to genotyping and DNA analysis FH
 key Location/Qualifiers
 FT source 1..11
 ATURES Location/Qualifiers
 source 1..11
 /organism="Homo sapiens (human)".
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

Query Match 30.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 8 TACGTGTACA 17
 1 TAGGTGTACA 10

RESULT 127
 LOCUS AR301464 11 bp DNA linear PAT 12-JUN-2003
 DEFINITION Sequence 45 from patent US 6538173.
 ACCESSION AR301464
 VERSION AR301464.1 GI:31689266
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 11)
 AUTHORS Heber-Katz, E.
 TITLE Compositions and methods for wound healing
 JOURNAL Patent: US 6538173-A 45 25-MAR-2003;
 FEATURES Location/Qualifiers
 source 1..11
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 30.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 12 TGTACGGGGA 21
 10 TGTACGGGGA 1

RESULT 128
 LOCUS K099043 11 bp DNA linear PAT 02-APR-2001
 DEFINITION Sequence 106 from Patent WO0120026.
 ACCESSION K099043
 VERSION K099043.1 GI:13538253
 KEYWORDS Synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Wojnowski, L. and Huster, E.
 TITLE Polymorphisms in the human hpxr gene and their use in diagnostic
 and therapeutic applications
 JOURNAL Patent: WO 0120026-A 106 22-MAR-2001;
 Epidauros Biotechnologie AG (DE)
 FEATURES Location/Qualifiers
 source 1..11
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="artificial sequence"

Query Match 30.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 18 GGGAGTCCAG 27
 2 GGGAGTGCAG 11

RESULT 129
 LOCUS AX099044 11 bp DNA linear PAT 02-APR-2001
 DEFINITION Sequence 107 from Patent WO0120026.
 ACCESSION AX099044
 VERSION AX099044.1 GI:13538254
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Wojnowski, L. and Huster, E.
 TITLE Polymorphisms in the human hpxr gene and their use in diagnostic
 and therapeutic applications
 JOURNAL Patent: WO 0120026-A 107 22-MAR-2001;
 Epidauros Biotechnologie AG (DE)
 FEATURES Location/Qualifiers
 source 1..11
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="artificial sequence"

Query Match 30.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 18 GGGAGTCCAG 27
 10 GGGAGTGCAG 1

RESULT 130
 LOCUS AX470626 11 bp DNA linear PAT 09-AUG-2002
 DEFINITION Sequence 203 from Patent WO02053773.
 ACCESSION AX470626
 VERSION AX470626.1 GI:22205751
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 REFERENCE 1
 AUTHORS Hofmann, K., Conrad, M. and Petersohn, D.
 TITLE Method for determining skin stress or skin ageing in vitro
 JOURNAL Patent: WO 02053773-A 203 11-JUL-2002;
 HENKEL KGAA (DE)
 FEATURES Location/Qualifiers
 source 1..11
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 30.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 13 GTACGGGAG 22
 10 GTTACGGGAG 1

RESULT 131


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X470645
OCUS      AX470645      11 bp      DNA      linear      PAT 09-AUG-2002
DEFINITION Sequence 222 from Patent WO02053773.
CESSION   AX470645
VERSION   AX470645.1 GI:22205770
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
TITLE     Method for determining skin stress or skin ageing in vitro
JOURNAL   HENKEL KGAA (DE)
FEATURES   Location/Qualifiers
            source          1..11
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"

Query Match      30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 CGGCGCCCTAC 10
   |||||
b 1 CGGCGCCCTAC 10

RESULT 132
X470757
OCUS      AX470757      11 bp      DNA      linear      PAT 09-AUG-2002
DEFINITION Sequence 334 from Patent WO02053773.
CESSION   AX470757
VERSION   AX470757.1 GI:22205882
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
TITLE     Method for determining skin stress or skin ageing in vitro
JOURNAL   HENKEL KGAA (DE)
FEATURES   Location/Qualifiers
            source          1..11
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"

Query Match      30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 18 GGGAGTCCAG 27
   |||||
b 2 GGGAGTCCAG 11

RESULT 133
X470853
OCUS      AX470853      11 bp      DNA      linear      PAT 09-AUG-2002
DEFINITION Sequence 430 from Patent WO02053773.
CESSION   AX470853
VERSION   AX470853.1 GI:22205978
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1

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AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
TITLE     Method for determining skin stress or skin ageing in vitro
JOURNAL   HENKEL KGAA (DE)
FEATURES   Location/Qualifiers
            source          1..11
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"

Query Match      30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 19 GGGAGTCCAGG 28
   |||||
b 2 GGGAGTCCAGG 11

RESULT 134
AX471193/c
LOCUS     AX471193      11 bp      DNA      linear      PAT 09-AUG-2002
DEFINITION Sequence 770 from Patent WO02053773.
CESSION   AX471193
VERSION   AX471193.1 GI:22206318
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
TITLE     Method for determining skin stress or skin ageing in vitro
JOURNAL   HENKEL KGAA (DE)
FEATURES   Location/Qualifiers
            source          1..11
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"

Query Match      30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 16 CAGGGAGTCC 25
   |||||
b 11 CAGTGAGTCC 2

RESULT 135
AX472098
LOCUS     AX472098      11 bp      DNA      linear      PAT 09-AUG-2002
DEFINITION Sequence 89 from Patent WO02053775.
CESSION   AX472098
VERSION   AX472098.1 GI:22207139
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Hustert,E., Haberl,M. and Wojnowski,L.
TITLE     Identification of the genetic determinants of the polymorphic
          cyp3a5 expression
JOURNAL   Patent: WO 02053775-A 89 11-JUL-2002;
          EPIDAUROS BIOTECHNOLOGIE AG (DE)
FEATURES   Location/Qualifiers
            source          1..11
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"

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Query Match      30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

13 GTACAGGAG 22
|||||
1 GTACAGGAG 10

SULT 136
623332
CUS AX623332 11 bp DNA linear PAT 21-FEB-2003
FINITION Sequence 373 from Patent WO02053774.
CSION AX623332
RSION AX623332.1 GI:28451273
WORDS
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 373 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

4 GCCCTACG 13
|||||
1 GCCCTACG 10

SULT 137
623370/c
CUS AX623370 11 bp DNA linear PAT 21-FEB-2003
FINITION Sequence 411 from Patent WO02053774.
CSION AX623370
RSION AX623370.1 GI:28451311
WORDS
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 411 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

18 GGGAGTCCAG 27
|||||
11 GGGAGTCCAG 2

SULT 138
623664/c
CUS AX623664 11 bp DNA linear PAT 21-FEB-2003
FINITION Sequence 705 from Patent WO02053774.
CSION AX623664
RSION AX623664.1 GI:28451605
WORDS
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 705 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

11 GTGTACAGG 20
|||||
11 GAGTACAGG 2

RESULT 139
AX623917
LOCUS AX623917 11 bp DNA linear PAT 21-FEB-2003
FINITION Sequence 958 from Patent WO02053774.
CSION AX623917
RSION AX623917.1 GI:28451858
WORDS
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 958 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

19 GGAGTCCAGG 28
|||||
2 GGATCCAGG 11

RESULT 140
AX624031/c
LOCUS AX624031 11 bp DNA linear PAT 21-FEB-2003
FINITION Sequence 1072 from Patent WO02053774.
CSION AX624031
RSION AX624031.1 GI:28451972
WORDS
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.

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TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1072 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES

source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 13 GTACAGGAG 22
| | | | |
b 10 GTTCAGGAG 1

RESULT 141

LOCUS AX624952 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1993 from Patent WO02053774.
ACCESSION AX624952
VERSION AX624952.1 GI:28452893
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1993 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES

source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 CGGGCCCTAC 10
| | | | |
b 1 CCGGCCCTAC 10

RESULT 142

LOCUS AX625222 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2263 from Patent WO02053774.
ACCESSION AX625222
VERSION AX625222.1 GI:28453163
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2263 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES

source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 9 ACGGTACAG 18
| | | | |
Db 11 AGGTGTACAG 2

RESULT 143

LOCUS AX625736 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2777 from Patent WO02053774.
ACCESSION AX625736
VERSION AX625736.1 GI:28453677
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2777 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES

source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 GGGAGTCCAG 27
| | | | |
Db 2 GGGACTCCAG 11

RESULT 144

LOCUS AX627101 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4142 from Patent WO02053774.
ACCESSION AX627101
VERSION AX627101.1 GI:28455139
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4142 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES

source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GTGTACAGG 20
| | | | |
Db 2 GTGTTCAGG 11

RESULT 145

LOCUS AX629184 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6225 from Patent WO02053774.

FEATURES	source	Henkel Kommanditgesellschaft auf Aktien (DE)
LOCUS	1. 11	Location/Qualifiers
DEFINITION	/organism="Homo sapiens"	
ACCESSION	/mol_type="unassigned DNA"	
VERSION	/db_xref="taxon:9606"	
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
FEATURES		
source		
LOCUS	AX630753	11 bp DNA linear PAT 21-FEB-2003
DEFINITION	Sequence 7794 from Patent WO02053774.	
ACCESSION	AX630753	
VERSION	AX630753.1 GI:28458791	
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	Petersohn,D., Conradt,M. and Hofmann,K.	
TITLE	Method for determining homeostasis of the skin	
JOURNAL	Patent: WO 02053774-A 7794 11-JUL-2002;	
FEATURES		
source		
LOCUS	AX630791	11 bp DNA linear PAT 21-FEB-2003
DEFINITION	Sequence 7832 from Patent WO02053774.	
ACCESSION	AX630791	
VERSION	AX630791.1 GI:28458831	
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	Petersohn,D., Conradt,M. and Hofmann,K.	
TITLE	Method for determining homeostasis of the skin	
JOURNAL	Patent: WO 02053774-A 7832 11-JUL-2002;	
FEATURES		
source		
LOCUS	AX630791/c	11 bp DNA linear PAT 21-FEB-2003
DEFINITION	Sequence 7832 from Patent WO02053774.	
ACCESSION	AX630791	
VERSION	AX630791.1 GI:28458831	
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	Petersohn,D., Conradt,M. and Hofmann,K.	
TITLE	Method for determining homeostasis of the skin	
JOURNAL	Patent: WO 02053774-A 7832 11-JUL-2002;	
FEATURES		
source		
LOCUS	AX630791/c	11 bp DNA linear PAT 21-FEB-2003
DEFINITION	Sequence 7832 from Patent WO02053774.	
ACCESSION	AX630791	
VERSION	AX630791.1 GI:28458831	
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	Petersohn,D., Conradt,M. and Hofmann,K.	
TITLE	Method for determining homeostasis of the skin	
JOURNAL	Patent: WO 02053774-A 7832 11-JUL-2002;	
FEATURES		
source		
LOCUS	AX630791/c	11 bp DNA linear PAT 21-FEB-2003
DEFINITION	Sequence 7832 from Patent WO02053774.	
ACCESSION	AX630791	
VERSION	AX630791.1 GI:28458831	
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	Petersohn,D., Conradt,M. and Hofmann,K.	
TITLE	Method for determining homeostasis of the skin	
JOURNAL	Patent: WO 02053774-A 7832 11-JUL-2002;	
FEATURES		
source		
LOCUS	AX630791/c	11 bp DNA linear PAT 21-FEB-2003
DEFINITION	Sequence 7832 from Patent WO02053774.	
ACCESSION	AX630791	
VERSION	AX630791.1 GI:28458831	
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	Petersohn,D., Conradt,M. and Hofmann,K.	
TITLE	Method for determining homeostasis of the skin	
JOURNAL	Patent: WO 02053774-A 7832 11-JUL-2002;	
FEATURES		
source		
LOCUS	AX630791/c	11 bp DNA linear PAT 21-FEB-2003
DEFINITION	Sequence 7832 from Patent WO02053774.	
ACCESSION	AX630791	
VERSION	AX630791.1 GI:28458831	
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	Petersohn,D., Conradt,M. and Hofmann,K.	
TITLE	Method for determining homeostasis of the skin	
JOURNAL	Patent: WO 02053774-A 7832 11-JUL-2002;	
FEATURES		
source		
LOCUS	AX630791/c	11 bp DNA linear PAT 21-FEB-2003
DEFINITION	Sequence 7832 from Patent WO02053774.	
ACCESSION	AX630791	
VERSION	AX630791.1 GI:28458831	
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	Petersohn,D., Conradt,M. and Hofmann,K.	
TITLE	Method for determining homeostasis of the skin	
JOURNAL	Patent: WO 02053774-A 7832 11-JUL-2002;	
FEATURES		
source		
LOCUS	AX630791/c	11 bp DNA linear PAT 21-FEB-2003
DEFINITION	Sequence 7832 from Patent WO02053774.	
ACCESSION	AX630791	
VERSION</		

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Y 18 GGGAGTCCAG 27
b 11 GGGAGTCCAG 2

RESULT 150
XG31085/c
LOCUS AX631085 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8126 from Patent WO02053774.
ACCESSION AX631085
VERSION AX631085.1 GI:28459129
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 8126 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 11 GTGTACAGG 20
b 11 GAGTACAGG 2

RESULT 151
XG31338
LOCUS AX631338 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8380 from Patent WO02053774.
ACCESSION AX631338
VERSION AX631338.1 GI:28459384
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 8380 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 19 GGGAGTCCAG 28
b 2 GGAATCCAG 11

RESULT 152
XG31452/c
LOCUS AX631452 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8494 from Patent WO02053774.
ACCESSION AX631452
VERSION AX631452.1 GI:28459518
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 9685 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 8494 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 13 GTACAGGAG 22
b 10 GTTCAGGAG 1

RESULT 153
XG32373
LOCUS AX632373 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9415 from Patent WO02053774.
ACCESSION AX632373
VERSION AX632373.1 GI:28467988
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 9415 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 CGGGCCCTAC 10
b 1 CCGGCCCTAC 10

RESULT 154
XG32643/c
LOCUS AX632643 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9685 from Patent WO02053774.
ACCESSION AX632643
VERSION AX632643.1 GI:28469258
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 9685 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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source

1. .11
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 30.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

9 ACGGTGACAG 18

|||||
 11 ACGGTGACAG 2

SULT 155
 124214/c
 CUS 11 bp DNA linear PAT 18-SEP-2002
 FINITION Compositions and method for healing wound.

BD124214

BD124214

BD124214.1 GI:23219159

BD124214.1 GI:23219159

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BD124214.1 GI:23219159

COMMENT

SOD CONSEILS RECH APPLIC (FR)
 Other publication CN 1124142 960612
 Other publication CZ 950168 960515
 Other publication BR 9503015 960604
 Other publication NZ 272398 960426
 Other publication HU 72133 960328
 Other publication JP 851985 960227
 Other publication FR 2721930 960105
 Other publication FR 2721827 960105
 Other publication FI 953170 951230
 Other publication SE 9502259 951230
 Other publication PL 309384 960108
 Other publication NO 952601 960102
 Other publication AU 2329995 960111
 Other publication CA 2152233 951230
 Other publication GB 2290791 960110.

FEATURES

source

1. .12
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"

Query Match 30.0%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 1.3e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 ACGGTGACAG 18

|||||

Db 11 ACGGTGACAG 2

RESULT 157

AR024089

LOCUS

AR024089

DEFINITION

Sequence 39 from patent US 5795778.

ACCESSION

AR024089

VERSION

AR024089.1 GI:3977383

KEYWORDS

Unknown.

SOURCE

Unknown.

REFERENCE

Unclassified.

1 (bases 1 to 12)

AUTHORS

Draper, K.G.

TITLE

Method and reagent for inhibiting herpes simplex virus replication

JOURNAL

Patent: US 5795778-A 39 18-AUG-1998;

FEATURES

Location/Qualifiers

source

1. .12

/organism="unknown"

/mol_type="unassigned DNA"

Query Match 30.0%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 1.3e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCTTACGTGT 14

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Db 1 CCCGACGTGT 10

RESULT 158

AR027886/c

LOCUS

AR027886

DEFINITION

Sequence 28 from patent US 5856461.

ACCESSION

AR027886

VERSION

AR027886.1 GI:5938706

KEYWORDS

Unknown.

SOURCE

Unknown.

REFERENCE

Unclassified.

1 (bases 1 to 12)

AUTHORS

Colote, S. and Pirotzky, E.

TITLE

Oligonucleotides to inhibit the expression of isoprenyl protein transferases

source

1. .11
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 30.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.1e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

9 ACGGTGACAG 18

|||||
 11 ACGGTGACAG 2

SULT 155
 124214/c
 CUS 11 bp DNA linear PAT 18-SEP-2002
 FINITION Compositions and method for healing wound.

BD124214

BD124214

BD124214.1 GI:23219159

BD124214.1 GI:23219159

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BD124214.1 GI:23219159

TITLE Oligonucleotide mediated nucleic acid recombination
JOURNAL
PATENT: JP 2002534966-A 25 22-OCT-2002;

MMENT
OS Homo sapiens (human)

PN JP 2002534966-A/25

PD 22-OCT-2002

PF 18-JAN-2000 JP 2000594068

PR 19-JAN-1999 US 60/116447, 05-FEB-1999 US 60/118813 PR

OS 05-FEB-1999 US 60/118854, 24-JUN-1999 US 60/141049 PR

PD 28-SEP-1999 US 09/408392, 28-SEP-1999 US 09/408393 PR

PF 12-OCT-1999 US 09/416375, 12-OCT-1999 US 09/416837 PI

PI ANDREAS CRAMER, WILLEM P C STENNER, JEREMY MINSHULL, STEVEN H PI

PC BASS,

PI MARK WELCH, JON E NESS, CLAES GUSTAFSSON, PHILLIP A PATTEN PC

PC C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N7/00, C12Q1/ PC

PC C12N5/00

CC Oligonucleotide mediated nucleic acid recombination PH Key

FT CDS Location/Qualifiers

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/organism="Homo sapiens"

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Query Match 30.0%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. 1.3e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

18 GGGAGTCCAG 27

2 GGGGTCCAG 11

RESULT 164

9627/c

LOCUS 12 bp DNA linear PAT 18-JUN-2001

DEFINITION Method for amplifying DNA fragment, method for estimating state of

microorganism existing and method for estimating state of waste.

ACCESSION E29627.1 GI:13021130

KEYWORDS JP 1999276176-A/107.

ORGANISM unidentified

unclassified.

REFERENCE 1 (bases 1 to 12)

Koichi, I.

Method for amplifying DNA fragment, method for estimating state of

microorganism existing and method for estimating state of waste

PATENT: JP 1999276176-A 107 12-OCT-1999;

SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE

FORESTRY AND FISHERIES

OS Unidentified

PN JP 1999276176-A/107

PD 12-OCT-1999

PF 31-MAR-1998 JP 1999087652

PR KOICHI INOUE

PC C12N15/09, B09B3/00, C12Q1/00, C12Q1/68, C12N15/00, B09B3/00 CC

Strandedness: Single; Location/Qualifiers

PH Key

FT source

1. .12

/organism="Unidentified".

Location/Qualifiers

1. .12

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/db_xref="taxon:32644"

Query Match 30.0%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. 1.3e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

18 GGGAGTCCAG 27

2 GGGGTCCAG 11

RESULT 164

9627/c

LOCUS 12 bp DNA linear PAT 18-JUN-2001

DEFINITION Method for amplifying DNA fragment, method for estimating state of

microorganism existing and method for estimating state of waste

PATENT: JP 1999276176-A 107 12-OCT-1999;

SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE

FORESTRY AND FISHERIES

OS Unidentified

PN JP 1999276176-A/107

PD 12-OCT-1999

PF 31-MAR-1998 JP 1999087652

PR KOICHI INOUE

PC C12N15/09, B09B3/00, C12Q1/00, C12Q1/68, C12N15/00, B09B3/00 CC

Strandedness: Single; Location/Qualifiers

PH Key

FT source

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/organism="Unidentified".

Location/Qualifiers

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Query Match 30.0%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. 1.3e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 CTACGTGTAC 16

Db 12 CTTCGTGTAC 3

RESULT 165

E38733/c

LOCUS 12 bp DNA linear PAT 31-JAN-2002

DEFINITION Method and device for amplifying DNA fragment.

ACCESSION E38733

VERSION E38733.1 GI:18621395

KEYWORDS JP 2000270867-A/107.

SOURCE unidentified

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 12)

Inoue, K.

Method and device for amplifying DNA fragment

PATENT: JP 2000270867-A 107 03-OCT-2000;

SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE

FORESTRY AND FISHERIES

OS Unidentified

PN JP 2000270867-A/107

PD 03-OCT-2000

PF 19-MAR-1999 JP 1999076844

PR KOICHI INOUE

PC C12N15/09, C12M1/00, C12Q1/68, C12N15/00

Strandedness: Single;

CC Topology: Linear;

PH Key

FT source

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/organism="Unidentified".

Location/Qualifiers

1. .12

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Query Match 30.0%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. 1.3e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

7 CTACGTGTAC 16

12 CTTCGTGTAC 3

RESULT 166

E64159/c

LOCUS 12 bp DNA linear PAT 18-JUN-2001

DEFINITION Method for amplifying DNA fragment, amplification apparatus of DNA

fragment, method for assaying a group of microorganisms, method

for analyzing a group of microorganisms, and method for assaying

contaminating substance.

E64159

E64159.1 GI:13019563

KEYWORDS JP 1999341989-A/107.

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 12)

Koichi, I.

Method for amplifying DNA fragment, amplification apparatus of DNA

fragment, method for assaying a group of microorganisms, method for

analyzing a group of microorganisms, and method for assaying

contaminating substance

PATENT: JP 1999341989-A 107 14-DEC-1999;

SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE

FORESTRY AND FISHERIES

OS Artificial Sequence

PN JP 1999341989-A/107


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PD 14-DEC-1999
PF 16-MAR-1999 JP 1999069694
PR
PI KOICHI INOUE
PC C12N15/09,C12M1/00,C12Q1/68,C12N15/00
CC
FH Key 1 Location/Qualifiers
FT source
FT Location/Qualifiers
   1..12
   /organism="Artificial Sequence".

FEATURES
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   1..12
   /organism="synthetic construct"
   /mol_type="genomic DNA"
   /db_xref="taxon:32630"

Query Match
Best Local Similarity 30.0%; Score 8.4; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 7 CTACGGTGATC 16
  ||| |||||
  12 CTTCGGTGATC 3

RESULT 167
LOCUS AR205443 12 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 25 from patent US 636861.
ACCESSION AR205443
VERSION AR205443.1 GI:21503026
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Cramer,A., Stemmer,W.P.C., Minshull,J., Bass,S.H., Welch,M.,
Ness,J.E., Gustafsson,C. and Patten,P.A.
TITLE Oligonucleotide mediated nucleic acid recombination
JOURNAL Patent: US 636861-A 25 09-APR-2002;
FEATURES
   source
   1..12
   /organism="unknown"
   /mol_type="unassigned DNA"

Query Match
Best Local Similarity 30.0%; Score 8.4; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 18 GGGAGTCCAG 27
  ||| |||||
  2 GGGGGTCCAG 11

RESULT 168
LOCUS AR220135 12 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 25 from patent US 6423542.
ACCESSION AR220135
VERSION AR220135.1 GI:23324577
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Cramer,A., Stemmer,W.P.C., Minshull,J., Bass,S.H., Welch,M.,
Ness,J.E., Gustafsson,C. and Patten,P.A.
TITLE Oligonucleotide mediated nucleic acid recombination
JOURNAL Patent: US 6423542-A 25 23-JUL-2002;
FEATURES
   source
   1..12
   /organism="unknown"
   /mol_type="genomic DNA"

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Query Match
Best Local Similarity 30.0%; Score 8.4; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 GGGAGTCCAG 27
  ||| |||||
  2 GGGGGTCCAG 11

Db

RESULT 169
LOCUS AR221524 12 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 25 from patent US 6426224.
ACCESSION AR221524
VERSION AR221524.1 GI:23328574
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Cramer,A., Stemmer,W.P.C., Minshull,J., Bass,S.H., Welch,M.,
Ness,J.E., Gustafsson,C. and Patten,P.A.
TITLE Oligonucleotide mediated nucleic acid recombination
JOURNAL Patent: US 6426224-A 25 30-JUL-2002;
FEATURES
   source
   1..12
   /organism="unknown"
   /mol_type="genomic DNA"

Query Match
Best Local Similarity 30.0%; Score 8.4; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 GGGAGTCCAG 27
  ||| |||||
  2 GGGGGTCCAG 11

Db

RESULT 170
LOCUS AR224308 12 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 39 from patent US 6440719.
ACCESSION AR224308
VERSION AR224308.1 GI:23333085
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting herpes simplex virus replication
JOURNAL Patent: US 6440719-A 39 27-AUG-2002;
FEATURES
   source
   1..12
   /organism="unknown"
   /mol_type="genomic DNA"

Query Match
Best Local Similarity 30.0%; Score 8.4; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCTACGTGT 14
  ||| |||||
  1 CCCGACGTGT 10

Db

RESULT 171
LOCUS AR254226 12 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 25 from patent US 6479652.
ACCESSION AR254226
VERSION AR254226.1 GI:27302963
KEYWORDS

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URCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Crameri,A., Stemmer,W.P.C., Minshull,J., Bass,S.H., Welch,M.,
Ness,J.E., Gustafsson,C. and Patten,P.A.
TITLE Oligonucleotide mediated nucleic acid recombination
JOURNAL Patent: US 6479652-A 25 12-NOV-2002;
FEATURES
    source
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            /organism="unknown"
            /mol_type="genomic DNA"

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

18 GGGAGTCCAG 27
|||||
2 GGGGGTCCAG 11

SULT 172
282432
CUS AR282432 12 bp DNA linear PAT 10-APR-2003
FINITION Sequence 25 from patent US 6521453.
CESSION AR282432
RSION AR282432.1 GI:29718598
WORDS
URCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Crameri,A., Stemmer,W.P.C., Minshull,J., Bass,S.H., Welch,M.,
Ness,J.E., Gustafsson,C. and Patten,P.A.
TITLE Oligonucleotide mediated nucleic acid recombination
JOURNAL Patent: US 6521453-A 25 18-FEB-2003;
FEATURES
    source
        1..12
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

18 GGGAGTCCAG 27
|||||
2 GGGGGTCCAG 11

SULT 173
1368339
CUS AR368339 12 bp DNA linear PAT 12-SEP-2003
FINITION Sequence 25 from patent US 6376246.
CESSION AR368339
RSION AR368339.1 GI:34602023
WORDS
URCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Crameri,A., Stemmer,W.P.C., Minshull,J., Bass,S.H., Welch,M.,
Ness,J.E., Gustafsson,C. and Patten,P.A.
TITLE Oligonucleotide mediated nucleic acid recombination
JOURNAL Patent: US 6376246-A 25 23-APR-2002;
FEATURES
    source
        1..12
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

18 GGGAGTCCAG 27
|||||
2 GGGGGTCCAG 11

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Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 GGGAGTCCAG 27
|||||
DB 2 GGGGGTCCAG 11

RESULT 174
AX463121/c
LOCUS AX463121 12 bp DNA linear PAT 15-JUL-2002
DEFINITION Sequence 4 from Patent WO0250108.
ACCESSION AX463121
VERSION AX463121.1 GI:21886102
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Marchal,G., Pescher,P. and Romain,F.
TITLE Immunogenic glycopeptides, screening, preparation and uses
JOURNAL Patent: WO 0250108-A 4 27-JUN-2002;
PASTEUR INSTITUT (FR)
FEATURES
    source
        1..12
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGCCTACGT 12
|||||
DB 12 GGCCCAAGT 3

RESULT 175
AX711090
LOCUS AX711090 12 bp RNA linear PAT 11-APR-2003
DEFINITION Sequence 390 from Patent EP1288296.
ACCESSION AX711090
VERSION AX711090.1 GI:29787471
KEYWORDS Herpes simplex virus unknown type
SOURCE Herpes simplex virus unknown type
ORGANISM Herpes simplex virus unknown type
REFERENCE 1
AUTHORS Draper,K.G., McSwiggen,J.A., Holecck,J.J., Dudycz,L.W.,
Macejak,D.G. and Mamone,J.A.
TITLE Method and reagent for inhibiting HBV viral replication
JOURNAL Patent: EP 1288296-A 390 05-MAR-2003;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
    source
        1..12
            /organism="Herpes simplex virus unknown type"
            /mol_type="unassigned RNA"
            /db_xref="taxon:126283"

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCCTACGTGT 14
|||||
DB 1 CCCGACGTGT 10

RESULT 176
BD001193
LOCUS BD001193 12 bp RNA linear PAT 31-JAN-2002
DEFINITION Method and reagent for inhibiting viral replication.

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```

CESSION BD001193
ERSON BD001193.1 GI:18625752
YWORDS JP 2000342285-A/353.
OURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 12)
AUTHORS Draper,K.G., Dadykztz,L.W., Macswigen,J.A., Maysejak,D.G.,
Holesek,J.V. and Mamone,A.J.
TITLE Method and reagent for inhibiting viral replication
JOURNAL Patent: JP 2000342285-A 353 12-DEC-2000;
RIBOZYME PHARMACEUTICALS INC
OMMENT OS Artificial Sequence
PN JP 2000342285-A/353
PD 12-DEC-2000
PF 01-MAY-2000 JP 2000132616
PR 11-MAY-1992 US 07/882689,14-MAY-1992 US 07/882712 PR
14-MAY-1992 US 07/882713,14-MAY-1992 US 07/882714 PR
14-MAY-1992 US 07/882823,14-MAY-1992 US 07/882824 PR
14-MAY-1992 US 07/882886,14-MAY-1992 US 07/882888 PR
14-MAY-1992 US 07/882889,14-MAY-1992 US 07/882921 PR
14-MAY-1992 US 07/882922,14-MAY-1992 US 07/883823 PR
14-MAY-1992 US 07/883849,14-MAY-1992 US 07/884073 PR
14-MAY-1992 US 07/884074,14-MAY-1992 US 07/884333 PR
14-MAY-1992 US 07/884422,14-MAY-1992 US 07/884431 PR
14-MAY-1992 US 07/884436,14-MAY-1992 US 07/884521 PR
31-JUL-1992 US 07/923738,26-AUG-1992 US 07/935854 PR
26-AUG-1992 US 07/936086,18-SEP-1992 US 07/948359 PR
15-OCT-1992 US 07/963322,07-DEC-1992 US 07/987129 PR
KENNETH G DRAPER,LEC W DADYKZT,JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,
PI JAMES J HOLESEK,ANTHONY J MAMONE
PC C12N15/09,C12N5/10,C12N7/00//A61K38/43,A61K39/125,A61K39/13,
PC A61K39/135,
PC A61K39/145,A61K39/21,A61K39/23,A61K39/245,A61K39/29,A61K48/00,
PC A61P1/16,
PC A61P31/14,A61P31/16,A61P31/18,A61P31/22,A61P35/02,C12O1/68,PC
(C12N15/09,C12R1:93),C12N15/00,C12N5/00,A61K37/48,(C12N15/00,PC
C12R1:93)
CC
FT Key Location/Qualifiers
FT source 1..12
FT /organism='Artificial Sequence'.
FEATURES
source
Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 CCTACGTGT 14
Db 1 CCCGACGTGT 10
RESULT 178
AR165205/c
LOCUS AR165205 21 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 19 from patent US 6274708.
ACCESSION AR165205
VERSION AR165205.1 GI:16238680
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Hilton,D.James.
TITLE Mouse interleukin-11 receptor
JOURNAL Patent: US 6274708-A 19 14-AUG-2001;
FEATURES
source
Query Match 29.3%; Score 8.2; DB 1; Length 21;
Best Local Similarity 76.9%; Pred. No. 2.8e+02;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 7 CTACGTGTACAGG 19
Db 15 CTCCTACGTACAGG 3

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SULT 179
456625/c
CUS AX456625 9 bp DNA linear PAT 06-JUL-2002
FINITION Sequence 97 from Patent WO0218407.
CESSION AX456625
RSTION AX456625.1 GI:21715512
YWORDS
URCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
          Eukaryota; Chordata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
1
REFERENCE Kurreck, J. and Erdmann, V.A.
AUTHORS
TITLE Antisense oligonucleotides against vrl
JOURNAL Patent: WO 0218407-A 97 07-MAR-2002;
          Gruenenthal GmbH (DE)
FEATURES
          Location/Qualifiers
            1..9
              /organism="Rattus norvegicus"
              /mol_type="genomic DNA"
              /db_xref="taxon:10116"
Query Match 28.6%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
19 GGAGTCCA 26
|||||
9 GGAGTCCA 2
SULT 180
668649/c
CUS AX668649 9 bp DNA linear PAT 26-MAR-2003
FINITION Sequence 2098 from Patent WO0242459.
CESSION AX668649
RSTION AX668649.1 GI:29291624
YWORDS
URCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
1
REFERENCE Liu, Q.
AUTHORS
TITLE Position dependent recognition of gnm nucleotide triplets by zinc
JOURNAL Patent: WO 0242459-A 2195 30-MAY-2002;
          Sangamo Biosciences Inc. (US)
FEATURES
          Location/Qualifiers
            1..9
              /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"
              /note="example target DNA"
Query Match 28.6%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
5 CCCTACGT 12
|||||
9 CCCTACGT 2
SULT 181
668651/c
CUS AX668651 9 bp DNA linear PAT 26-MAR-2003
FINITION Sequence 2100 from Patent WO0242459.
CESSION AX668651
RSTION AX668651.1 GI:29291626
YWORDS
URCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
1
REFERENCE Liu, Q.
AUTHORS
TITLE Position dependent recognition of gnm nucleotide triplets by zinc
JOURNAL Patent: WO 0242459-A 2453 30-MAY-2002;
          Sangamo Biosciences Inc. (US)
FEATURES
          Location/Qualifiers
            1..9
              /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"
              /note="example target DNA"
Query Match 28.6%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
5 CCCTACGT 12
|||||
9 CCCTACGT 2

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artificial sequences.
1
REFERENCE Liu, Q.
AUTHORS
TITLE Position dependent recognition of gnm nucleotide triplets by zinc
JOURNAL Patent: WO 0242459-A 2100 30-MAY-2002;
          Sangamo Biosciences Inc. (US)
FEATURES
          Location/Qualifiers
            1..9
              /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"
              /note="example target DNA"
Query Match 28.6%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
5 CCCTACGT 12
|||||
9 CCCTACGT 2
RESULT 182
AX668746
LOCUS AX668746 9 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 2195 from Patent WO0242459.
ACCESSION AX668746
VERSION AX668746.1 GI:29291721
KEYWORDS
SOURCE synthetic construct
          synthetic construct
          artificial sequences.
1
REFERENCE Liu, Q.
AUTHORS
TITLE Position dependent recognition of gnm nucleotide triplets by zinc
JOURNAL Patent: WO 0242459-A 2195 30-MAY-2002;
          Sangamo Biosciences Inc. (US)
FEATURES
          Location/Qualifiers
            1..9
              /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"
              /note="example target DNA"
Query Match 28.6%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
17 AGGAGTC 24
|||||
2 AGGAGTC 9
RESULT 183
AX669004/c
LOCUS AX669004 9 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 2453 from Patent WO0242459.
ACCESSION AX669004
VERSION AX669004.1 GI:29291981
KEYWORDS
SOURCE synthetic construct
          synthetic construct
          artificial sequences.
1
REFERENCE Liu, Q.
AUTHORS
TITLE Position dependent recognition of gnm nucleotide triplets by zinc
JOURNAL Patent: WO 0242459-A 2453 30-MAY-2002;
          Sangamo Biosciences Inc. (US)
FEATURES
          Location/Qualifiers
            1..9

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 10)
 Hoffmann, S.J. and Nagai, K.
 TITLE Blood substitutes
 JOURNAL Patent: US 5661124-A 12 26-AUG-1997;
 FEATURES Location/Qualifiers
 source 1..10
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 28.6%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CGGCGCCT 8
 |||||
 b 3 CGGCGCCT 10

RESULT 191
 LOCUS AR274316 10 bp DNA linear PAT 10-APR-2003
 DEFINITION Sequence 12 from patent US 5506561.
 ACCESSION AR274316
 VERSION AR274316.1 GI:29706762
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED

REFERENCE 1 (bases 1 to 10)
 Cheval, J., Elalouf, J.-M. and Virlon, B.
 TITLE Method of obtaining a library of tags capable of defining a
 specific state of a biological sample
 JOURNAL Patent: US 6506561-A 12 14-JAN-2003;
 FEATURES Location/Qualifiers
 source 1..10
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 28.6%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 17 AGGAGTC 24
 |||||
 b 9 AGGAGTC 2

RESULT 192
 LOCUS AX033036 10 bp DNA linear PAT 21-SEP-2000
 DEFINITION Sequence 11 from Patent EP1024201.
 ACCESSION AX033036
 VERSION AX033036.1 GI:10279939
 KEYWORDS
 SOURCE Mus sp.
 ORGANISM Mus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 REFERENCE 1
 Elalouf, J.M., Cheval, J. and Virlon, B.
 TITLE Microassay for serial analysis of gene expression and applications
 thereof
 JOURNAL Patent: EP 1024201-A 11 02-AUG-2000;
 COMMISSARIAT ENERGIE ATOMIQUE (FR) ; DE CENTRE NAT (FR)
 FEATURES Location/Qualifiers
 source 1..10
 /organism="Mus sp."
 /mol_type="unassigned DNA"
 /db_xref="taxon:10095"

Query Match 28.6%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 AGGAGTC 24
 |||||
 Db 9 AGGAGTC 2

RESULT 193
 LOCUS AX104933 10 bp DNA linear PAT 30-APR-2001
 DEFINITION Sequence 1125 from Patent WO0122972.
 ACCESSION AX104933
 VERSION AX104933.1 GI:13921130
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 Krieg, A.M., Schetter, C. and Vollmer, J.C.
 AUTHORS Immunostimulatory nucleic acids
 TITLE Patent: WO 0122972-A 1125 05-APR-2001;
 JOURNAL UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
 GmbH (DE)
 FEATURES Location/Qualifiers
 source 1..10
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"

Query Match 28.6%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ACGTGTC 16
 |||||
 Db 1 ACGTGTC 8

RESULT 194
 LOCUS AX152549 10 bp DNA linear PAT 22-JUN-2001
 DEFINITION Sequence 464 from Patent WO0138577.
 ACCESSION AX152549
 VERSION AX152549.1 GI:14534200
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
 AUTHORS Human transcriptomes
 TITLE Patent: WO 0138577-A 464 31-MAY-2001;
 JOURNAL The Johns Hopkins University (US)
 FEATURES Location/Qualifiers
 source 1..10
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 28.6%; Score 8; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 AGTCCAGG 28
 |||||
 Db 10 AGTCCAGG 3

RESULT 195
 LOCUS AX152759 10 bp DNA linear PAT 22-JUN-2001
 DEFINITION Sequence 674 from Patent WO0138577.
 ACCESSION AX152759

FEATURES	source	1. .10	Location/Qualifiers
		/organism="Homo sapiens"	
		/mol_type="unassigned DNA"	
		/db_xref="taxon:9606"	
Query Match		28.6%; Score 8; DB 1; Length 10;	
Best Local Similarity		100.0%; Pred. No. 1.1e+02;	
Matches		8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY		9 ACGGTAC 16	
DB		10 ACGGTAC 3	
RESULT 198			
AX374632			
LOCUS		AX374632	10 bp DNA linear PAT 01-MAR-2002
DEFINITION		Sequence 53 from Patent WO0210454.	
ACCESSION		AX374632	
VERSION		AX374632.1	GI:19169529
KEYWORDS			
SOURCE			Homo sapiens (human)
ORGANISM			Homo sapiens
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
			Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE			
AUTHORS			Choi, J. Y., Koshy, B., Klien, S. and Stephens, J. C.
TITLE			Haplotypes of the alas2 gene.
JOURNAL			Patent: WO 0210454-A 53 07-FEB-2002;
			Genaissance Pharmaceuticals, Inc. (US)
FEATURES			Location/Qualifiers
		1. .10	
		/organism="Homo sapiens"	
		/mol_type="unassigned DNA"	
		/db_xref="taxon:9606"	
Query Match		28.6%; Score 8; DB 1; Length 10;	
Best Local Similarity		100.0%; Pred. No. 1.1e+02;	
Matches		8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY		21 AGTCCAGG 28	
DB		2 AGTCCAGG 9	
RESULT 199			
BD007893			
LOCUS		BD007893	10 bp DNA linear PAT 31-JAN-2002
DEFINITION		LPS activated human monocyte expressing genes.	
ACCESSION		BD007893	
VERSION		BD007893.1	GI:18632666
KEYWORDS		JP 2001069993-A/169,	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE			
AUTHORS			Matsushima, K., Hashimoto, S. and Suzuki, T.
TITLE			LPS activated human monocyte expressing genes
JOURNAL			Patent: JP 2001069993-A 169 21-MAR-2001;
			JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT			OS Homo sapiens (human)
			FN JP 2001069993-A/169
			PD 21-MAR-2001
			PF 28-APR-2000 JP 2000131079
PR			
PI			KUJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI PC
			CI2N15/09, C07K14/47, C07K15/18, G01N33/50, G01N33/53//A61K45/00, PC
			A61P29/00.
PC			A61P31/00, C12P21/08, C12N15/00
CC			
CC			
PH			
Key			Location/Qualifiers

FEATURES	source
Velculescu,V.E., Vogelstein,B. and Kinzler,K.W. Characterization of the yeast transcriptome Patent: JP 2001509017-A 209 10-JUL-2001; THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE OS Saccharomyces cerevisiae (yeast) PN JP 2001509017-A/209 PD 10-JUL-2001 PR 22-JAN-1998 JP 1998532117 PP 23-JAN-1997 US 60/035917 FI VICTOR E VELCULESCU,BERT VOGELSTEIN,KENNETH W KINZLER PC C12N15/10,C12N15/31,C07K14/395,C12Q1/68,C12Q1/02 CC Characterization of the yeast transcriptome FH Key Location/Qualifiers FT source 1..10 /organism='Saccharomyces cerevisiae (yeast)'. Location/Qualifiers 1..10 /organism='Saccharomyces cerevisiae' /mol_type='genomic DNA' /db_xref='taxon:4932'	
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13 GTACAGGG 20	
1 GTACAGGG 8	
RESULT 202	
008083323/c	
OCUCS	10 bp DNA linear PAT 27-AUG-2002
DEFINITION	Human matured/activated dendritic cell expression genes.
ACCESSION	EB083323
VERSION	EB083323.1 GI:22628933
KEYWORDS	JP 2001327293-A/244.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 10)
TITLE	Matsumura K., Hashimoto S., Suzuki T. and Nagai S.
JOURNAL	Human matured/activated dendritic cell expression genes
COMMENT	Patent: JP 2001327293-A 244.27-NOV-2001; JAPAN SCIENCE AND TECHNOLOGY CORP OS Homo sapiens (human) PN JP 2001327293-A/244 PD 27-NOV-2001 PP 22-MAY-2000 JP 2000150562 PI KOJI MATSUMURA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI NAGAI PC C12N15/09,C07K14/47,C07K16/18/C12P21/02,C12P21/08,C12N15/00 CC
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Best Local Similarity	100.0%; Pred.No. 1.1e+02;
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
11 GTGTACAG 18	
9 GTGTACAG 2	
RESULT 203	
D167068	
OCUCS	10 bp DNA linear PAT 17-JAN-2001

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FINITION Human liver disease-expressing genes.
CESSION BD167068 1 GI:27872880
REGION BD167068 1 GI:27872880
WORDS JP 2002209591-A/613.
JRC unclassified
JRCISM unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 613 30-JUL-2002;
JOURNAL JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PD JP 2002209591-A/613
PI 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
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/mol_type='genomic DNA'
/db_xref='taxon:32644'

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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
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1 CGGGCCCT 8
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3 CGGGCCCT 10

RESULT 204
LOCUS BD167170 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD167170
VERSION BD167170.1 GI:27872982
KEYWORDS unclassified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 715 30-JUL-2002;
JOURNAL JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PD JP 2002209591-A/715
PI 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
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/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 28.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGGGCCCT 8
|||||
3 CGGGCCCT 10

RESULT 204
LOCUS BD167170 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD167170
VERSION BD167170.1 GI:27872982
KEYWORDS unclassified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 715 30-JUL-2002;
JOURNAL JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PD JP 2002209591-A/715
PI 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
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FT /organism='Homo sapiens (human)'.
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/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCCT 8
DB 3 CGGGCCCT 10

RESULT 205
LOCUS AR282864 11 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 9 from patent US 6524792.
ACCESSION AR282864
VERSION AR282864.1 GI:29719666
KEYWORDS Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Renner W.A., Orberger, G.H., Koller, D. and Bailey, J.E.
TITLE Expression cloning processes for the discovery, characterization
and isolation of genes encoding polypeptides with a predetermined
property
JOURNAL Patent: US 6524792-A 9 25-FEB-2003;
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1..11
/organism='unknown'
/mol_type='genomic DNA'

Query Match 28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCCT 8
DB 4 CGGGCCCT 11

RESULT 206
LOCUS AX393110 11 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 40 from Patent WO0210217.
ACCESSION AX393110
VERSION AX393110.1 GI:19701160
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS St Croix,B., Kinzler,K.W. and Vogelstein,B.
TITLE Endothelial cell expression patterns
JOURNAL Patent: WO 0210217-A 40 07-FEB-2002;
JOURNAL The Johns Hopkins University (US)
FEATURES
source
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/organism='Homo sapiens'
/mol_type='unassigned DNA'
/db_xref='taxon:9606'

Query Match 28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCCCTAC 10
DB 1 GGCCCTAC 8

RESULT 207
AX421267

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OCUS AX421267 11 bp DNA linear PAT 18-JUN-2002
EFINITION Sequence 15 from Patent WO0218641.
CESSION AX421267
ERISION AX421267.1 GI:21524675
EYWORDS synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Risinger,C., Andersson,M.K., Lewander,T. and Olaisson,E.
TITLE Detection of cyp3a4 and cyp2c9 polymorphisms
JOURNAL Patent: WO 0218641-A 15 07-MAR-2002;
Gemin Genomics PLC (GB)
EATURES Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide of the novel polymorphic site 461
on the coding strand"
Query Match 28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
y 11 GTGTACAG 18
| | | | |
b 3 GTGTACAG 10
RESULT 208
AX421268/c
OCUS 11 bp DNA linear PAT 18-JUN-2002
EFINITION Sequence 16 from Patent WO0218641.
CESSION AX421268
ERISION AX421268.1 GI:21524676
EYWORDS synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Risinger,C., Andersson,M.K., Lewander,T. and Olaisson,E.
TITLE Detection of cyp3a4 and cyp2c9 polymorphisms
JOURNAL Patent: WO 0218641-A 16 07-MAR-2002;
Gemin Genomics PLC (GB)
EATURES Location/Qualifiers
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/note="Oligonucleotide of the novel polymorphic site 461
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
y 11 GTGTACAG 18
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b 9 GTGTACAG 2
RESULT 209
AX470469/c
OCUS 11 bp DNA linear PAT 09-AUG-2002
EFINITION Sequence 46 from Patent WO02053773.
CESSION AX470469
ERISION AX470469.1 GI:22205594
EYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 46 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
Query Match 28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
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QY 21 AGTCCAGG 28
| | | | |
Db 10 AGTCCAGG 3
RESULT 210
AX470788
LOCUS 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 365 from Patent WO02053773.
ACCESSION AX470788
VERSION AX470788.1 GI:22205913
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 365 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES Location/Qualifiers
1..11
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/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 19 GGAGTCCA 26
| | | | |
Db 2 GGAGTCCA 9
RESULT 211
AX470933/c
LOCUS 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 510 from Patent WO02053773.
ACCESSION AX470933
VERSION AX470933.1 GI:22206058
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 510 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

20 GAGTCCAG 27
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11 GAGTCCAG 4

SULT 212
471363
CUS AX471363 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 940 from Patent WO02053773.
ACCESSION AX471363
VERSION AX471363.1 GI:22206488
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Hofmann,K., Conradt,M. and Petersohn,D.
AUTHORS Method for determining skin stress or skin ageing in vitro
TITLE Patent: WO 02053773-A 940 11-JUL-2002;
JOURNAL Henkel KGAA (DE)
FEATURES
Location/Qualifiers
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Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
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18 GGGAGTCC 25
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4 GGGAGTCC 11

SULT 213
471851
CUS AX471851 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 1428 from Patent WO02053773.
ACCESSION AX471851
VERSION AX471851.1 GI:22206976
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Hofmann,K., Conradt,M. and Petersohn,D.
AUTHORS Method for determining skin stress or skin ageing in vitro
TITLE Patent: WO 02053773-A 1428 11-JUL-2002;
JOURNAL HENKEL KGAA (DE)
FEATURES
Location/Qualifiers
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1. .11
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Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

19 GGAGTCCA 26
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3 GGAGTCCA 10

SULT 214
4623060

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LOCUS AX623060 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 101 from Patent WO02053774.
ACCESSION AX623060
VERSION AX623060.1 GI:28451001
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 101 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
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Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

15 ACAGGGAG 22
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2 ACAGGGAG 9

RESULT 215
AX623555/c
LOCUS AX623555 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 596 from Patent WO02053774.
ACCESSION AX623555
VERSION AX623555.1 GI:28451496
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 596 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
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21 AGTCCAGG 28
|||||
11 AGTCCAGG 4

RESULT 216
AX624143
LOCUS AX624143 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1184 from Patent WO02053774.
ACCESSION AX624143
VERSION AX624143.1 GI:28452084
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS

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TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 1184 11-JUL-2002; (DE)
           Henkel Kommanditgesellschaft auf Aktien (DE)
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 12 TGTACAGG 19
b 4 TGTACAGG 11

RESULT 217
X625138/c
OCUS      X625138
DEFINITION Sequence 2179 from Patent WO02053774.
ACCESSION AX625138
VERSION   AX625138.1 GI:28453079
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 2179 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 20 GAGTCCAG 27
b 11 GAGTCCAG 4

RESULT 218
X625188/c
OCUS      X625188
DEFINITION Sequence 2229 from Patent WO02053774.
ACCESSION AX625188
VERSION   AX625188.1 GI:28453129
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 2229 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;

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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTACGTGT 14
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DB 11 CTACGTGT 4

RESULT 219
X625450
LOCUS      X625450
DEFINITION Sequence 2491 from Patent WO02053774.
ACCESSION AX625450
VERSION   AX625450.1 GI:28453391
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 2491 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
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      /mol_type="unassigned DNA"
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Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCCTACG 11
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DB 4 GCCCTACG 11

RESULT 220
X625464/c
LOCUS      X625464
DEFINITION Sequence 2505 from Patent WO02053774.
ACCESSION AX625464
VERSION   AX625464.1 GI:28453405
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 2505 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGCCCTA 9
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DB 9 GGGCCCTA 2

RESULT 221
X625855
LOCUS      X625855
DEFINITION Sequence 2896 from Patent WO02053774.

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CESSION      AX625855      1  GI:28453893
RSION
YWORDS
URCE
ORGANISM      Homo sapiens (human)
              Homo sapiens
              Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 2896 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
SOURCE
  1. .11
  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"
Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 1.3e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

20 GAGTCCAG 27
|||||
4 GAGTCCAG 11

SULT 222
626664
CUS
FINITION      Sequence 3705 from Patent WO02053774.
CESSION
RSION
YWORDS
URCE
ORGANISM      Homo sapiens (human)
              Homo sapiens
              Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 3705 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
SOURCE
  1. .11
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  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"
Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 1.3e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

18 GGGAGTCC 25
|||||
4 GGGAGTCC 11

SULT 223
627013
CUS
FINITION      Sequence 4054 from Patent WO02053774.
CESSION
RSION
YWORDS
URCE
ORGANISM      Homo sapiens (human)
              Homo sapiens
              Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 4054 11-JUL-2002;

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FEATURES
SOURCE
  1. .11
  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"
Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 1.3e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 GGGCCCTA 9
|||||
3 GGGCCCTA 10

RESULT 224
AX627782/c
LOCUS
DEFINITION      Sequence 4823 from Patent WO02053774.
ACCESSION
VERSION
KEYWORDS
SOURCE
  Homo sapiens (human)
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 4823 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
SOURCE
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  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"
Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 1.3e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

21 AGTCCAGG 28
|||||
10 AGTCCAGG 3

RESULT 225
AX629261/c
LOCUS
DEFINITION      Sequence 6302 from Patent WO02053774.
ACCESSION
VERSION
KEYWORDS
SOURCE
  Homo sapiens (human)
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 6302 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
SOURCE
  1. .11
  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"
Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 1.3e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

21 AGTCCAGG 28
|||||
10 AGTCCAGG 3

RESULT 225
AX629261/c
LOCUS
DEFINITION      Sequence 6302 from Patent WO02053774.
ACCESSION
VERSION
KEYWORDS
SOURCE
  Homo sapiens (human)
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 6302 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
SOURCE
  1. .11
  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"
Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 1.3e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Y      15 ACAGGGAG 22
b      11 ACAGGGAG 4

RESULT 226
X629639
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 6680 from Patent WO02053774.
ACCESSION AX629639
VERSION   AX629639.1 GI:28457677
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 6680 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
           source
             1..11
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      19 GGAGTCCA 26
b      2 GGAGTCCA 9

RESULT 227
X629743/c
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 6784 from Patent WO02053774.
ACCESSION AX629743
VERSION   AX629743.1 GI:28457781
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 6784 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
           source
             1..11
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      20 GAGTCCAG 27
b      9 GAGTCCAG 2

RESULT 228
X630481
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 7522 from Patent WO02053774.
ACCESSION AX630481
VERSION   AX630481.1 GI:28458519
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 7522 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers

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KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 7522 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
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             1..11
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      15 ACAGGGAG 22
b      2 ACAGGGAG 9

RESULT 229
X630976/c
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 8017 from Patent WO02053774.
ACCESSION AX630976
VERSION   AX630976.1 GI:28459018
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 8017 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
           source
             1..11
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match      28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y      21 AGTCCAGG 28
b      11 AGTCCAGG 4

RESULT 230
X631564
LOCUS      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 8606 from Patent WO02053774.
ACCESSION AX631564
VERSION   AX631564.1 GI:28459640
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 8606 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers

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source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 28.6%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

12 TGTACAGG 19
|||||
4 TGTACAGG 11

SULT 231
632559/c
CUS
AX632559 11 bp DNA linear PAT 21-FEB-2003
Sequence 9601 from Patent WO02053774.
FINITION
CESSION
AX632559
RSTON
AX632559.1 GI:28468174
YWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS
Method for determining homeostasis of the skin
TITLE
Patent: WO 02053774-A 9601 11-JUL-2002;
JOURNAL
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 28.6%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

20 GAGTCCAG 27
|||||
11 GAGTCCAG 4

SULT 232
632609/c
CUS
AX632609 11 bp DNA linear PAT 21-FEB-2003
Sequence 9651 from Patent WO02053774.
FINITION
CESSION
AX632609
RSTON
AX632609.1 GI:28468224
YWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS
Method for determining homeostasis of the skin
TITLE
Patent: WO 02053774-A 9651 11-JUL-2002;
JOURNAL
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 28.6%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

7 CTACGTGT 14
|||||

Db 11 CTACGTGT 4

RESULT 233
AX632794
LOCUS
AX632794 11 bp DNA linear PAT 21-FEB-2003
Sequence 9836 from Patent WO02053774.
ACCESSION
AX632794
VERSION
AX632794.1 GI:28468409
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS
Method for determining homeostasis of the skin
TITLE
Patent: WO 02053774-A 9836 11-JUL-2002;
JOURNAL
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 28.6%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 19 GGAGTCCA 26
|||||
3 GGAGTCCA 10

Db 3 GGAGTCCA 10

RESULT 234
I11566
LOCUS
I11566 12 bp DNA linear PAT 26-JUL-1995
Sequence 4 from Patent US 5407822.
ACCESSION
I11566
VERSION
I11566.1 GI:909084
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 12)
AUTHORS
Leplatris,P., Loison,G., Pessegue,B. and Shire,D.
TITLE
Artificial promoter for the expression of proteins in yeast
JOURNAL
Patent: US 5407822-A 4 18-APR-1995;
FEATURES
Location/Qualifiers
1. .12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 28.6%; Score 8; DB 1; Length 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGGGCCCT 8
|||||
5 CGGGCCCT 12

Db 5 CGGGCCCT 12

RESULT 235
I14185
LOCUS
I14185 12 bp DNA linear PAT 26-SEP-1995
Sequence 17 from patent US 5446138.
ACCESSION
I14185
VERSION
I14185.1 GI:996608
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 12)

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AUTHORS Blaiseu,P.-L., Legoux,R., Leguay,J.-J. and Schneider,M.
 TITLE Recombinant DNA coding for a protein with endochitinase activity
 JOURNAL Patent: US 5446138-A 17 29-AUG-1995;
 FEATURES Location/Qualifiers
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 1..12
 /organism="unknown"
 /mol_type="unassigned DNA"
 Query Match 28.6%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CGGGCCCT 8
 b 5 CGGGCCCT 12

RESULT 236
 AX711182
 LOCUS AX711182 12 bp DNA linear PAT 07-OCT-1996
 DEFINITION Sequence 15 from patent US 5545526.
 ACCESSION AX711182
 VERSION 124587
 KEYWORDS 124587.1 GI:1604457
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 12)
 AUTHORS Baxter-Lowe,L.Ann.
 TITLE Method for HLA Typing
 JOURNAL Patent: US 5545526-A 15 13-AUG-1996;
 FEATURES Location/Qualifiers
 source
 1..12
 /organism="unknown"
 /mol_type="unassigned DNA"
 Query Match 28.6%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CGGGCCCT 8
 b 9 CGGGCCCT 2

RESULT 237
 AX235321
 LOCUS AX235321 12 bp DNA linear PAT 11-SEP-2001
 DEFINITION Sequence 23 from Patent WO0162967.
 ACCESSION AX235321
 VERSION AX235321.1 GI:15593866
 KEYWORDS Hordeum vulgare
 SOURCE Hordeum vulgare
 ORGANISM Hordeum vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Hordeum.
 REFERENCE 1
 AUTHORS Vider,B.Z. and Katzir,N.
 TITLE A method that compares genomic sequences
 JOURNAL Patent: WO 0162967-A 23 30-AUG-2001;
 Genena Ltd. (IL); Agricultural Research Organization Neve Ya'ar
 Research Center (IL)
 FEATURES Location/Qualifiers
 source
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 /organism="Hordeum vulgare"
 /mol_type="unassigned DNA"
 /db_xref="taxon:4513"
 Query Match 28.6%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCTACGTG 13
 Db 1 CCTACGTG 8

RESULT 238
 AX711182
 LOCUS AX711182 17 bp DNA linear PAT 11-APR-2003
 DEFINITION Sequence 482 from Patent EP1288296.
 ACCESSION AX711182
 VERSION AX711182.1 GI:29787563
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Draper,K.G., Mcswiggen,J.A., Holecsek,J.J., Dudycz,L.W.,
 Macejak,D.G. and Mamane,J.A.
 TITLE Method and reagent for inhibiting HBV viral replication
 JOURNAL Patent: EP 1288296-A 482 05-MAR-2003;
 RIBOZYME PHARMACEUTICALS, INC. (US)
 FEATURES Location/Qualifiers
 source
 1..17
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Nucleic acid clone fragments"
 Query Match 28.6%; Score 8; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCCT 8
 Db 7 CGGGCCCT 14

RESULT 239
 AX625951
 LOCUS AX625951 11 bp DNA linear PAT 21-FEB-2003
 DEFINITION Sequence 2992 from Patent WO02053774.
 ACCESSION AX625951
 VERSION AX625951.1 GI:28453989
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
 TITLE Method for determining homeostasis of the skin
 JOURNAL Patent: WO 02053774-A 2992 11-JUL-2002;
 Henkel Kommanditgesellschaft auf Aktien (DE)
 FEATURES Location/Qualifiers
 source
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 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 Query Match 27.9%; Score 7.8; DB 1; Length 11;
 Best Local Similarity 81.8%; Pred. No. 1.5e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CTACGTGTACA 17
 Db 1 CTTCCTGTACA 11

RESULT 240
 AX472098/c
 LOCUS AX472098 11 bp DNA linear PAT 09-AUG-2002
 DEFINITION Sequence 89 from Patent WO02053775.
 ACCESSION AX472098

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RESULT 241
LOCUS AX472098.1 GI:22207139
DEFINITION Homo sapiens (human)
ACCESSION AR301655
VERSION AR301655.1
KEYWORDS
SOURCE
  1. .11
  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"

Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 6 CCTAGCTGAC 16
|||||
11 CTTCTCTGAC 1

RESULT 242
LOCUS AR301655
DEFINITION Sequence 4 from patent US 5474897.
ACCESSION I16095
VERSION I16095.1 GI:1251003
KEYWORDS
SOURCE
  1. .11
  /organism="unknown"
  /mol_type="unassigned DNA"

Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 16 CAGGAGTCCA 26
|||||
1 CAGAGATTCCA 11

RESULT 243
LOCUS AR301691/c
DEFINITION Sequence 272 from patent US 6538173.
ACCESSION AR301691
VERSION AR301691.1 GI:31689493
KEYWORDS
SOURCE
  Unknown.
  ORGANISM
    Unclassified.
  REFERENCE
    1 (bases 1 to 11)
    Heber-Katz, E.
  AUTHORS
    Heber-Katz, E.
  TITLE
    Compositions and methods for wound healing
  JOURNAL
    Patent: US 6538173-A 272 25-MAR-2003;
  FEATURES
    Location/Qualifiers
      1. .11
      source
        /organism="unknown"
        /mol_type="genomic DNA"

Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 11 GGGGCCCCAGG 11
|||||

RESULT 244
LOCUS AX470747
DEFINITION Sequence 324 from Patent WO02053773.
ACCESSION AX470747
VERSION AX470747.1 GI:22205872
KEYWORDS
SOURCE
  Homo sapiens (human)
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1
    Hofmann, K., Conrad, M. and Petersohn, D.
  AUTHORS
    Hofmann, K., Conrad, M. and Petersohn, D.
  TITLE
    Method for determining skin stress or skin ageing in vitro
  JOURNAL
    Patent: WO 02053773-A 324 11-JUL-2002;
  FEATURES
    Location/Qualifiers
      1. .11
      source
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 16 CAGGAGTCCA 26
|||||
11 CAGAGAGGCCA 11

RESULT 245
LOCUS AX470906/c
DEFINITION Sequence 236 from patent US 6538173.
ACCESSION AR301655
VERSION AR301655.1 GI:31689457
KEYWORDS
SOURCE
  Unknown.
  ORGANISM
    Unclassified.
  REFERENCE
    1 (bases 1 to 11)
    Heber-Katz, E.
  AUTHORS
    Heber-Katz, E.
  TITLE
    Compositions and methods for wound healing
  JOURNAL
    Patent: US 6538173-A 236 25-MAR-2003;
  FEATURES
    Location/Qualifiers
      1. .11
      source
        /organism="unknown"

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/mol_type="genomic DNA"

Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 18 GGGAGTCCAGG 28
|||||
1 GGGGCCCCAGG 11

RESULT 243
LOCUS AR301691/c
DEFINITION Sequence 272 from patent US 6538173.
ACCESSION AR301691
VERSION AR301691.1 GI:31689493
KEYWORDS
SOURCE
  Unknown.
  ORGANISM
    Unclassified.
  REFERENCE
    1 (bases 1 to 11)
    Heber-Katz, E.
  AUTHORS
    Heber-Katz, E.
  TITLE
    Compositions and methods for wound healing
  JOURNAL
    Patent: US 6538173-A 272 25-MAR-2003;
  FEATURES
    Location/Qualifiers
      1. .11
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Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 10 CGTGTACAGGG 20
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11 CTTGTACAGGG 11

RESULT 244
LOCUS AX470747
DEFINITION Sequence 324 from Patent WO02053773.
ACCESSION AX470747
VERSION AX470747.1 GI:22205872
KEYWORDS
SOURCE
  Homo sapiens (human)
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1
    Hofmann, K., Conrad, M. and Petersohn, D.
  AUTHORS
    Hofmann, K., Conrad, M. and Petersohn, D.
  TITLE
    Method for determining skin stress or skin ageing in vitro
  JOURNAL
    Patent: WO 02053773-A 324 11-JUL-2002;
  FEATURES
    Location/Qualifiers
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        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 16 CAGGAGTCCA 26
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11 CAGAGAGGCCA 11

RESULT 245
LOCUS AX470906/c
DEFINITION Sequence 236 from patent US 6538173.
ACCESSION AR301655
VERSION AR301655.1 GI:31689457
KEYWORDS
SOURCE
  Unknown.
  ORGANISM
    Unclassified.
  REFERENCE
    1 (bases 1 to 11)
    Heber-Katz, E.
  AUTHORS
    Heber-Katz, E.
  TITLE
    Compositions and methods for wound healing
  JOURNAL
    Patent: US 6538173-A 236 25-MAR-2003;
  FEATURES
    Location/Qualifiers
      1. .11
      source
        /organism="unknown"

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DEFINITION Sequence 483 from Patent WO02053773.
ACCESSION AX470906
VERSION AX470906.1 GI:22206031
FEATURES
  SOURCE Homo sapiens (human)
  ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
  AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE Method for determining skin stress or skin ageing in vitro
  JOURNAL Patent: WO 02053773-A 483 11-JUL-2002;
  HENKEL KGAA (DE)
FEATURES
  SOURCE Location/Qualifiers
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    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"
  Query Match 27.9%; Score 7.8; DB 1; Length 11;
  Best Local Similarity 81.8%; Pred. No. 1.5e+02;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
  Y 2 GGCCCTTGT 12
  b 11 GGCCCTTGT 1
RESULT 246
AX470952/c
OCUS AX470952 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 529 from Patent WO02053773.
ACCESSION AX470952
VERSION AX470952.1 GI:22206077
FEATURES
  SOURCE Homo sapiens (human)
  ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
  AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE Method for determining skin stress or skin ageing in vitro
  JOURNAL Patent: WO 02053773-A 529 11-JUL-2002;
  HENKEL KGAA (DE)
FEATURES
  SOURCE Location/Qualifiers
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    /db_xref="taxon:9606"
  Query Match 27.9%; Score 7.8; DB 1; Length 11;
  Best Local Similarity 81.8%; Pred. No. 1.5e+02;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
  Y 16 CAGGGAGTCCA 26
  b 11 CAGGGAGTCCA 1
RESULT 247
AX471524
OCUS AX471524 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 1101 from Patent WO02053773.
ACCESSION AX471524
VERSION AX471524.1 GI:22206649
FEATURES
  SOURCE Homo sapiens (human)
  ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
  AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE Method for determining skin stress or skin ageing in vitro

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JOURNAL Patent: WO 02053773-A 1101 11-JUL-2002;
  HENKEL KGAA (DE)
FEATURES
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    /db_xref="taxon:9606"
  Query Match 27.9%; Score 7.8; DB 1; Length 11;
  Best Local Similarity 81.8%; Pred. No. 1.5e+02;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
  QY 11 GTGTACAGGA 21
  Db 1 GTGTAAATGGA 11
RESULT 248
AX471669/c
LOCUS AX471669 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 1246 from Patent WO02053773.
ACCESSION AX471669
VERSION AX471669.1 GI:22206794
FEATURES
  SOURCE Homo sapiens (human)
  ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
  AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE Method for determining skin stress or skin ageing in vitro
  JOURNAL Patent: WO 02053773-A 1246 11-JUL-2002;
  HENKEL KGAA (DE)
FEATURES
  SOURCE Location/Qualifiers
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"
  Query Match 27.9%; Score 7.8; DB 1; Length 11;
  Best Local Similarity 81.8%; Pred. No. 1.5e+02;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
  QY 18 GGGACTCCAGG 28
  Db 11 GGGACTGCAGG 1
RESULT 249
AX471699/c
LOCUS AX471699 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 1276 from Patent WO02053773.
ACCESSION AX471699
VERSION AX471699.1 GI:22206824
FEATURES
  SOURCE Homo sapiens (human)
  ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
  AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE Method for determining skin stress or skin ageing in vitro
  JOURNAL Patent: WO 02053773-A 1276 11-JUL-2002;
  HENKEL KGAA (DE)
FEATURES
  SOURCE Location/Qualifiers
  1..11
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"
  Query Match 27.9%; Score 7.8; DB 1; Length 11;
  Best Local Similarity 81.8%; Pred. No. 1.5e+02;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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VERSION AX624024.1 GI:28451965
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 1065 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
          source
            1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 18 GGGAGTCCAGG 28
DB 11 GGGATTTCAGG 1
RESULT 253
AX624330/c
LOCUS AX624330 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1371 from Patent WO02053774.
ACCESSION AX624330
VERSION AX624330.1 GI:28452271
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 1371 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
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              /db_xref="taxon:9606"
Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 18 GGGAGTCCAGG 28
DB 11 GGGATTTCAGG 1
RESULT 254
AX624837/c
LOCUS AX624837 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1878 from Patent WO02053774.
ACCESSION AX624837
VERSION AX624837.1 GI:28452778
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 1878 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)

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JUL 250
171796/c
CUS 5 CCTCAGTGTA 15
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      11 CCTCAGTGTA 1
AX471796 11 bp DNA linear PAT 09-AUG-2002
Sequence 1373 from Patent WO02053773.
FESSION AX471796
SION AX471796.1 GI:22206921
WORDS Homo sapiens (human)
ORCE Homo sapiens
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Hofmann,K., Conradt,M. and Petersohn,D.
AUTHORS Method for determining skin stress or skin ageing in vitro
TITLE Patent: WO 02053773-A 1373 11-JUL-2002;
JOURNAL HENKEL KGAA (DE)
FEATURES Location/Qualifiers
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              /db_xref="taxon:9606"
Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 16 CAGGGAGTCCA 26
DB 11 CGGGAGGCCA 1
RESULT 251
623640/c
CUS AX623640 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 681 from Patent WO02053774.
FESSION AX623640
SION AX623640.1 GI:28451581
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 681 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
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              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 18 GGGAGTCCAGG 28
DB 11 GGGATTCTAGG 1
RESULT 252
K624024/c
CUS AX624024 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1065 from Patent WO02053774.
FESSION AX624024

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    /db_xref="taxon:9606"

Query Match
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Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

y 18 GGGAGTCCAGG 28
b 11 GGGATACAGG 1

RESULT 255
LOCUS
  AX625047/c
  Sequence 2088 from Patent WO02053774.
  DEFINITION
  AX625047
  CESSION
  AX625047
  ERSION
  AX625047.1 GI:28452988
  KEYWORDS
  Homo sapiens (human)
  ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
  1
  AUTHORS
  Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE
  Method for determining homeostasis of the skin
  JOURNAL
  Patent: WO 02053774-A 2088 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
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      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
  27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

y 18 GGGAGTCCAGG 28
b 11 GGTAGCCAGG 1

RESULT 256
LOCUS
  AX625403
  Sequence 2444 from Patent WO02053774.
  DEFINITION
  AX625403
  CESSION
  AX625403
  ERSION
  AX625403.1 GI:28453344
  KEYWORDS
  Homo sapiens (human)
  ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
  1
  AUTHORS
  Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE
  Method for determining homeostasis of the skin
  JOURNAL
  Patent: WO 02053774-A 2444 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
  FEATURES
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      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
  27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

y 17 AGGGAGTCCAG 27

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Db
  1 AGGGAGACCTG 11

RESULT 257
LOCUS
  AX625794
  Sequence 2835 from Patent WO02053774.
  DEFINITION
  AX625794
  CESSION
  AX625794.1 GI:28453735
  KEYWORDS
  Homo sapiens (human)
  SOURCE
  Homo sapiens
  ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
  1
  AUTHORS
  Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE
  Method for determining homeostasis of the skin
  JOURNAL
  Patent: WO 02053774-A 2835 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
  FEATURES
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Query Match
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Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

y 16 CAGGGAGTCCA 26
b 1 CAGGGGGTTCA 11

RESULT 258
LOCUS
  AX626034/c
  Sequence 3075 from Patent WO02053774.
  DEFINITION
  AX626034
  CESSION
  AX626034.1 GI:28454072
  KEYWORDS
  Homo sapiens (human)
  SOURCE
  Homo sapiens
  ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
  1
  AUTHORS
  Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE
  Method for determining homeostasis of the skin
  JOURNAL
  Patent: WO 02053774-A 3075 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
  FEATURES
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      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
  27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

y 16 CAGGGAGTCCA 26
b 11 CAGAGAGGCCA 1

RESULT 259
LOCUS
  AX626752
  Sequence 3793 from Patent WO02053774.
  DEFINITION
  AX626752
  CESSION
  AX626752.1 GI:28454790
  KEYWORDS

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URCE      Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 3793 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
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Query Match      27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

          2 GGGCCCTACGT 12
          |||||
          11 GGGCCCTTGT 1

RESULT 260
LOCUS      AX626783              11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3824 from Patent WO02053774.
ACCESSION  AX626783
VERSION    AX626783.1 GI:28454821
KEYWORDS   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 3824 11-JUL-2002; (DE)
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
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              /organism="Homo sapiens"
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              /db_xref="taxon:9606"
Query Match      27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

          18 GGGAGTCCAGG 28
          |||||
          11 GGGGTTCAGG 1

RESULT 261
LOCUS      AX626888              11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3929 from Patent WO02053774.
ACCESSION  AX626888
VERSION    AX626888.1 GI:28454926
KEYWORDS   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 3929 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
          source
            1..11

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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match      27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

          14 TACAGGGAGTC 24
          |||||
          1 TAATGGGAGTC 11

RESULT 262
LOCUS      AX627660              11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4701 from Patent WO02053774.
ACCESSION  AX627660
VERSION    AX627660.1 GI:28455698
KEYWORDS   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 4701 11-JUL-2002; (DE)
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
          source
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              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
Query Match      27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

          16 CAGGGAGTCCA 26
          |||||
          1 CAGTGATCCA 11

RESULT 263
LOCUS      AX627965              11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 5006 from Patent WO02053774.
ACCESSION  AX627965
VERSION    AX627965.1 GI:28456003
KEYWORDS   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 5006 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
          source
            1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
Query Match      27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

          11 GTGTACAGGGA 21
          |||||
          1 GTGTAATGGA 11

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RESULT 264
X628121/c
OCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
JOURNAL
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 5162 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 18 GGGAGTCCAGG 28
|||||
b 11 GGGACTGCAGG 1

RESULT 265
X628521/c
OCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
JOURNAL
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 5562 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 18 GGGAGTCCAGG 28
|||||
b 11 GGGACTGCAGG 1

RESULT 266
X628699/c
OCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
JOURNAL
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 5740 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Y 17 AGGAGTCCAG 27
|||||
b 11 AGGGAATCTAG 1

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REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 CAGGAGTCCA 26
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Db 11 CGGGGGGTCCA 1

RESULT 267
X629205
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 6246 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 ACAGGAGTCC 25
|||||
Db 1 ACAGGGTGACC 11

RESULT 268
X629571
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Petersohn,D., Conradt,M. and Hofmann,K.
Method for determining homeostasis of the skin
Patent: WO 02053774-A 6612 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 ACAGGAGTCC 25
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Db 1 ACAGGGTGACC 11

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/ db_xref="taxon:9606"

Query Match      27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 GGGCCCTTCTCT 12
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1 GGGCCCTTCTCT 11

SULT 269
629648
CUS AX629648 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6689 from Patent WO02053774.
ACCESSION AX629648
VERSION AX629648.1 GI:28457686
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 689 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

5 CCTACGCTGTA 15
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1 CCTACGCTGTA 11

SULT 270
629882/c
CUS AX629882 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6923 from Patent WO02053774.
ACCESSION AX629882
VERSION AX629882.1 GI:28457920
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6923 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

5 CCTACGCTGTA 15
|||||
1 CCTACGCTGTA 11

SULT 271
AX630279 11 bp DNA linear PAT 21-FEB-2003
LOCUS Sequence 7320 from Patent WO02053774.
DEFINITION AX630279
ACCESSION AX630279.1 GI:28458317
VERSION AX630279.1
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7320 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
/organism="Homo sapiens"
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Query Match      27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

18 GGGAGTCCAGG 28
|||||
1 GGGAGTCCAGG 11

SULT 272
AX631061/c
LOCUS Sequence 8102 from Patent WO02053774.
DEFINITION AX631061
ACCESSION AX631061.1 GI:28459103
VERSION AX631061.1
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8102 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
1..11
/organism="Homo sapiens"
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/db_xref="taxon:9606"

Query Match      27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

18 GGGAGTCCAGG 28
|||||
1 GGGAGTCCAGG 11

SULT 273
AX631445/c
LOCUS Sequence 8487 from Patent WO02053774.
DEFINITION AX631445
ACCESSION AX631445.1 GI:28459511
VERSION AX631445.1
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```


REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8487 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Y 18 GGGAGTCCAGG 28
|||||
b 11 GGGATTCCAGG 1
RESULT 274
X631751/c
OCUS X631751 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8793 from Patent WO02053774.
ACCESSION AX631751
VERSION AX631751.1 GI:28459858
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8793 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Y 18 GGGAGTCCAGG 28
|||||
b 11 GGGATTCCAGG 1
RESULT 275
X632258/c
OCUS X632258 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9300 from Patent WO02053774.
ACCESSION AX632258
VERSION AX632258.1 GI:28467873
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9300 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 18 GGGAGTCCAGG 28
|||||
DB 11 GGGATACAGG 1
RESULT 276
AX632468/c
LOCUS AX632468 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9510 from Patent WO02053774.
ACCESSION AX632468
VERSION AX632468.1 GI:28468083
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9510 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 18 GGGAGTCCAGG 28
|||||
DB 11 GGTAGGCCAGG 1
RESULT 277
BD124405
LOCUS BD124405 11 bp DNA linear PAT 18-SEP-2002
DEFINITION Compositions and method for healing wound.
ACCESSION BD124405
VERSION BD124405.1 GI:23219350
KEYWORDS JP 2002503460-A/236.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
AUTHORS Katz,E.H.
TITLE Compositions and method for healing wound
JOURNAL Patent: JP 2002503460-A 236 05-FEB-2002;
THE WISTAR INSTITUTE
COMMENT OS Mus musculus (mouse)
PN 2002503460-A/236
PD 05-FEB-2002
PF 13-FEB-1999 JP 2000531545
PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
28-SEP-1998 US 60/102051
PI ELLEN HESER KATZ
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
C12N5/00
CC Compositions and method for healing wound
FH Key Location/Qualifiers
FT source 1. .11
/organism="Mus musculus"
/mol_type="genomic DNA"
FEATURES
source
1. .11
/organism="Mus musculus"
/mol_type="genomic DNA"

<p>Other publication BR 9503015 960604 Other publication NZ 272398 960426 Other publication HU 72133 960328 Other publication JP 8051985 960327 Other publication FR 2721930 960105 Other publication FR 2721827 960105 Other publication FI 953170 951230 Other publication SE 9502259 951230 Other publication PL 309384 960108 Other publication NO 952601 960102 Other publication AU 232995 960111 Other publication CA 2152233 951230 Other publication GB 2290791 960110. Location/Qualifiers</p>					
<p>FEATURES source 1..12 /organism="unidentified" /mol_type="unassigned DNA" /db_xref="taxon:32644"</p>					
<p>Query Match 27.9%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 1.7e+02; Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;</p>					
QY	13 GTACAGGGAGT 23				
DB	11 GTCCAGAGAT 1				
<p>RESULT 280 A91496/c 12 bp DNA linear PAT 22-JAN-2000 LOCUS Sequence 23 from Patent WO9824928. DEFINITION A91496 ACCESSION A91496.1 GI:6740451 VERSION unidentified KEYWORDS unclassified SOURCE unclassified ORGANISM unclassified.</p>					
<p>REFERENCE AUTHORS Pallisgaard,N. and Hokland,P. TITLE DETECTION OF CHROMOSOMAL ABNORMALITIES JOURNAL Patent: WO 9824928-A 23 11-JUN-1998: PALLISGAARD NIELS (DK); HOKLAND PETER (DK) FEATURES source Location/Qualifiers 1..12 /organism="unidentified" /mol_type="unassigned DNA" /db_xref="taxon:32644"</p>					
<p>Query Match 27.9%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 1.7e+02; Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;</p>					
QY	7 CTACGTGTACA 17				
DB	11 CTCAGCCTACA 1				
<p>RESULT 281 AR027883/c 12 bp DNA linear PAT 29-SEP-1999 LOCUS Sequence 25 from patent US 5856461. DEFINITION AR027883 ACCESSION AR027883.1 GI:5938703 VERSION Unknown. KEYWORDS Unknown. SOURCE Unknown. ORGANISM Unclassified.</p>					
<p>REFERENCE AUTHORS Colote,S. and Pirozky,E. TITLE Oligonucleotides to inhibit the expression of isoprenyl protein transferases JOURNAL Patent: US 5856461-A 25 05-JAN-1999;</p>					

TITLE
Method for amplifying DNA fragment, amplification apparatus of DNA fragment, method for assaying a group of microorganisms, method for analyzing a group of microorganisms, and method for assaying contaminating substance

JOURNAL
Patent: JP 199341989-A 25 14-DEC-1999;
SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE FORESTRY AND FISHERIES

INVENTOR
OS Artificial Sequence
PN JP 199341989-A/25
PD 14-DEC-1999
PP 16-MAR-1999 JP 1999069694

INVENTOR
PR KOICHI INOUE
PI C12N15/09,C12M1/00,C12Q1/68,C12N15/00
CC

KEY
FH Key
FT source
FT Location/Qualifiers
1. .12
/organism="Artificial Sequence".

FEATURES
source
1. .12
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 27.9%; Score 7.8; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

7 CTGAGGTGACA 17
|||||
11 CTTGCTGTAGA 1

SULT 286
3754/c
CUS
FINITION
Sequence 19 from patent US 5538844.
123754
CESSION
123754.1 GI:1603624
YWORDS
Unknown.
ORGANISM
Unclassified.

REFERENCE
1 (bases 1 to 12)
AUTHORS
Duyao,M.P., MacDonald,M.E. and Gusella,J.F.
TITLE
Transport protein gene from the Huntington's disease region
JOURNAL
Patent: US 5538844-A 19 23-JUL-1996;
FEATURES
source
1. .12
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 27.9%; Score 7.8; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

5 GCCTACGTGTA 15
|||||
12 CCTACCTGAA 2

SULT 287
15021/c
CUS
FINITION
Sequence 107 from patent US 5599704.
135021
CESSION
135021.1 GI:2087989
YWORDS
Unknown.
ORGANISM
Unclassified.

REFERENCE
1 (bases 1 to 12)
AUTHORS
Thompson,J.D. and Draper,K.G.

TITLE
ErbB2/neu targeted ribozymes
JOURNAL
Patent: US 5599704-A 107 04-FEB-1997;
FEATURES
Location/Qualifiers
1. .12
/organism="unknown"
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Query Match
Best Local Similarity 27.9%; Score 7.8; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

4 GCCTACGTGT 14
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12 GCCTAGGTGT 2

RESULT 288
AR224412
LOCUS
Definition 9 from patent US 6440723.
12 bp RNA linear PAT 26-SEP-2002
AR224412
ACCESSION
AR224412.1 GI:23333191
VERSION
KEYWORDS
Unknown.
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 12)
AUTHORS
Dale,R.M.K.
TITLE
Arrays with modified oligonucleotide and polynucleotide compositions
JOURNAL
Patent: US 6440723-A 9 27-AUG-2002;
FEATURES
source
1. .12
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned RNA"

Query Match
Best Local Similarity 27.9%; Score 7.8; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

15 ACAGGGAGTCC 25
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1 ATAGGGATCC 11

RESULT 289
AX073604/c
LOCUS
Definition 26 from Patent WO0104320.
12 bp DNA linear PAT 06-FEB-2001
AX073604
ACCESSION
AX073604.1 GI:12710027
VERSION
KEYWORDS
synthetic construct
synthetic construct
artificial sequences.

REFERENCE
1
AUTHORS
Schmidt,A.C., Skiadopoulos,M.H., Collins,P.L., Murphy,B.R.,
Bailey,J.E. and Durbin,A.P.
TITLE
Attenuated human-bovine chimeric parainfluenza virus (piw) vaccines
JOURNAL
Patent: WO 0104320-A 26 18-JAN-2001;
THE GOVERNMENT OF THE UNITED STATES OF AMERICA (US)
FEATURES
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/note="Sequence flanking site for introduction of Bsi WI site for rHPIV3 S"

Query Match
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Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;


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COMMENT
PN JP 2001505428-A/23
PD 24-APR-2001
PF 08-DEC-1997 JP 1998525090
PI NEILLS PARISGARD,PATER HOKURANDO
PC C12N15/09,C12Q1/68,G01N33/50,C12N15/00
CC C12N15/09,C12Q1/68,G01N33/50,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC /desc = 'DNA (synthetic)';
FH Key Location/Qualifiers.

FEATURES
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        /db_xref="taxon:9606"

Query Match
Best Local Similarity 27.9%; Score 7.8; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

7 CTACGCTGCTACA 17
11 CTACGCTGCTACA 1

RESULT 295
AX690109/c
LOCUS AX690109/c 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 2841 from Patent EPI281758.
ACCESSION AX690109
VERSION AX690109.1 GI:29412967
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 2841 05-FEB-2003;
Aeomica, Inc. (US)
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        1..25
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        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
Best Local Similarity 27.9%; Score 7.8; DB 1; Length 25;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

4 GCCCTACGCTGTCACAGGAG 22
23 GCATCGCTGCACACGTAG 5

RESULT 296
AX690110/c
LOCUS AX690110/c 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 2842 from Patent EPI281758.
ACCESSION AX690110
VERSION AX690110.1 GI:29412968
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 2842 05-FEB-2003;
Aeomica, Inc. (US)
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        /db_xref="taxon:9606"

Query Match
Best Local Similarity 27.9%; Score 7.8; DB 1; Length 25;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

4 GCCCTACGCTGTCACAGGAG 22
23 GCATCGCTGCACACGTAG 5

RESULT 297
AX690107/c
LOCUS AX690107/c 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 2839 from Patent EPI281758.
ACCESSION AX690107
VERSION AX690107.1 GI:29412965
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 2839 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
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        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
Best Local Similarity 27.9%; Score 7.8; DB 1; Length 25;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

4 GCCCTACGCTGTCACAGGAG 22
22 GCATCGCTGCACACGTAG 4

RESULT 298
AX690108/c
LOCUS AX690108/c 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 2840 from Patent EPI281758.
ACCESSION AX690108
VERSION AX690108.1 GI:29412966
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 2840 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
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        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
Best Local Similarity 27.9%; Score 7.8; DB 1; Length 25;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

4 GCCCTACGCTGTCACAGGAG 22
25 GCATCGCTGCACACGTAG 7

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Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 Y 4 GCCTACGCTGACAGGAG 22
 b 24 GCCTCGCTGCACACGTAG 6

RESULT 299
 X690111/c
 OCUS AX690111 25 bp DNA linear PAT 31-MAR-2003
 DEFINITION Sequence 2843 from Patent EP1281758.
 CCSSION AX690111
 ERSION AX690111.1 GI:29412969
 EYWORDS
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
 JOURNAL Patent: EP 1281758-A 2843 05-FEB-2003;
 Aeomica, Inc. (US)
 FEATURES
 source 1..25
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 27.9%; Score 7.8; DB 1; Length 25;
 Best Local Similarity 63.2%; Pred.No.2.9e+02;
 Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Y 4 GCCTACGCTGACAGGAG 22
 b 21 GCCTCGCTGCACACGTAG 3

RESULT 300
 X690112/c
 OCUS AX690112 25 bp DNA linear PAT 31-MAR-2003
 DEFINITION Sequence 2844 from Patent EP1281758.
 CCSSION AX690112
 ERSION AX690112.1 GI:29412970
 EYWORDS
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
 JOURNAL Patent: EP 1281758-A 2844 05-FEB-2003;
 Aeomica, Inc. (US)
 FEATURES
 source 1..25
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 27.9%; Score 7.8; DB 1; Length 25;
 Best Local Similarity 63.2%; Pred.No.2.9e+02;
 Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Y 4 GCCTACGCTGACAGGAG 22
 b 20 GCCTCGCTGCACACGTAG 2

RESULT 301
 X096928/c

LOCUS AX096928 10 bp DNA linear PAT 30-MAR-2001
 DEFINITION Sequence 2106 from Patent WO0118250.
 ACCESSION AX096928
 VERSION AX096928.1 GI:13513196
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and Mccarthy,J.J.
 TITLE Single nucleotide polymorphisms in genes
 JOURNAL Patent: WO 0118250-A 2106 15-MAR-2001;
 WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium Pharmaceuticals, Inc. (US)
 FEATURES
 Location/Qualifiers
 source 1..10
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 27.1%; Score 7.6; DB 1; Length 10;
 Best Local Similarity 87.5%; Pred.No.1.3e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 ACAGGGAG 22
 Db 10 MCAGGGAG 3

Search completed: April 19, 2004, 14:25:26
 Job time : 2 secs

KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.

XX WO200253774-A2.
 XX 11-JUL-2002.
 XX 20-DEC-2001; 2001WO-EP015179.
 XX 03-JAN-2001; 2001DE-01000127.
 XX (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 XX WPI; 2002-590638/63.

XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.

XX Claim 24; Page 255; 1345pp; German.
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention

SQ Sequence 11 BP; 1 A; 4 C; 2 G; 4 T; 0 U; 0 Other;
 Query Match 28.6%; Score 8; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 AGTCCAGG 28
 DB 11 AGTCCAGG 4

RESULT 536
 ABV71814/C
 ID ABEV71814 standard; cDNA; 11 BP.

XX ABEV71814;
 XX 21-OCT-2002 (first entry)
 XX Human skin EST 9600.
 XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.

XX WO200253774-A2.
 XX 11-JUL-2002.
 XX 20-DEC-2001; 2001WO-EP015179.
 XX 03-JAN-2001; 2001DE-01000127.

XX (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 XX WPI; 2002-590638/63.
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.

XX Claim 24; Page 310; 1345pp; German.
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention

SQ Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 28.6%; Score 8; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 GAGTCCAG 27
 DB 11 GAGTCCAG 4

RESULT 537
 ABV62315
 ID ABEV62315 standard; cDNA; 11 BP.

XX ABEV62315;
 XX 21-OCT-2002 (first entry)
 XX Human skin EST 101.
 XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.

XX WO200253774-A2.
 XX 11-JUL-2002.
 XX 20-DEC-2001; 2001WO-EP015179.
 XX 03-JAN-2001; 2001DE-01000127.
 XX (HENK) HENKEL KGAA.
 XX Petersohn D, Conradt M, Hofmann K;
 XX WPI; 2002-590638/63.

XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.

XX Disclosure; Page 28; 1345pp; German.

CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 4 A; 2 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 ACAGGGAG 22
Db 2 ACAGGGAG 9

RESULT 538
ABV67037/C
ID ABV67037 standard; cDNA; 11 BP.
XX
AC ABV67037;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 4823.
XX
KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 158; 1345pp; German.
XX
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX

SQ Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 AGTCCAGG 28
Db 10 AGTCCAGG 3

RESULT 539
ABV70819
ID ABV70819 standard; cDNA; 11 BP.
XX
AC ABV70819;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 8605.
XX
KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Claim 24; Page 275; 1345pp; German.
XX
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 3 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TGACAGG 19
Db 4 TGACAGG 11

RESULT 540
ABV64705

ID ABV64705 standard; cDNA; 11 BP.
 XX AC ABV64705;
 XX DT 21-OCT-2002 (first entry)
 XX DE Human skin EST 2491.
 XX XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX OS Homo sapiens.
 XX PN WO200253774-A2.
 XX PD 11-JUL-2002.
 XX PF 20-DEC-2001; 2001WO-EP015179.
 XX PR 03-JAN-2001; 2001DE-01000127.
 XX PA (HENK) HENKEL KGAA.
 XX PI Petersohn D, Conradt M, Hofmann K;
 XX XX WPI; 2002-590638/63.
 XX PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX PS Disclosure; Page 94; 1345pp; German.
 XX CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX SQ Sequence 11 BP; 1 A; 6 C; 3 G; 1 T; 0 U; 0 Other;
 XX
 XX Query Match 28.6%; Score 8; DB 1; Length 11;
 XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 GCCTACG 11
 Db 4 GCCTACG 11
 RESULT 541
 ID ABV62810 standard; cDNA; 11 BP.
 XX AC ABV62810;
 XX DT 21-OCT-2002 (first entry)
 XX DE Human skin EST 596.
 XX XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX OS Homo sapiens.

XX PN WO200253774-A2.
 XX PD 11-JUL-2002.
 XX PF 20-DEC-2001; 2001WO-EP015179.
 XX PR 03-JAN-2001; 2001DE-01000127.
 XX PA (HENK) HENKEL KGAA.
 XX PI Petersohn D, Conradt M, Hofmann K;
 XX XX WPI; 2002-590638/63.
 XX PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX PS Disclosure; Page 41; 1345pp; German.
 XX CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX SQ Sequence 11 BP; 1 A; 4 C; 2 G; 4 T; 0 U; 0 Other;
 XX
 XX Query Match 28.6%; Score 8; DB 1; Length 11;
 XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 21 AGTCCAGG 28
 Db 11 AGTCCAGG 4
 RESULT 542
 ID ABV64719/c
 XX ID ABV64719 standard; cDNA; 11 BP.
 XX AC ABV64719;
 XX DT 21-OCT-2002 (first entry)
 XX DE Human skin EST 2505.
 XX XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX OS Homo sapiens.
 XX PN WO200253774-A2.
 XX PD 11-JUL-2002.
 XX PF 20-DEC-2001; 2001WO-EP015179.
 XX PR 03-JAN-2001; 2001DE-01000127.
 XX PA (HENK) HENKEL KGAA.
 XX PI Petersohn D, Conradt M, Hofmann K;
 XX XX

DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
XX
PS Disclosure; Page 94; 1345pp; German.
XX
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
XX Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
SQ
Query Match 28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGGCCCTA 9
DB 9 GGGCCCTA 2
RESULT 543
ABV65110
ID ABV65110 standard; cDNA; 11 BP.
XX
AC ABV65110;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 2896.
XX
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
OS
XX WO200253774-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-EP015179.
XX
XX 03-JAN-2001; 2001DE-01000127.
XX
XX (HENK) HENKEL KGAA.
XX
XX Petersohn D, Conradt M, Hofmann K;
PI
XX WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
XX Claim 24; Page 312; 1345pp; German.
XX
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
XX Sequence 11 BP; 5 A; 2 C; 3 G; 1 T; 0 U; 0 Other;
SQ
Query Match 28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 GAGTCCAG 27
DB 4 GAGTCCAG 11
RESULT 544
ABV71864/c
ID ABV71864 standard; cDNA; 11 BP.
XX
XX ABV71864;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 9650.
XX
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
OS
XX WO200253774-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-EP015179.
XX
XX 03-JAN-2001; 2001DE-01000127.
XX
XX (HENK) HENKEL KGAA.
XX
XX Petersohn D, Conradt M, Hofmann K;
PI
XX WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
XX Claim 24; Page 312; 1345pp; German.
XX
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
XX Sequence 11 BP; 5 A; 2 C; 3 G; 1 T; 0 U; 0 Other;
SQ
Query Match 28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 GAGTCCAG 27
DB 4 GAGTCCAG 11

CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
XX Sequence 11 BP; 3 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
SQ
Query Match 28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 GAGTCCAG 27
DB 4 GAGTCCAG 11
RESULT 544
ABV71864/c
ID ABV71864 standard; cDNA; 11 BP.
XX
XX ABV71864;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 9650.
XX
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
OS
XX WO200253774-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-EP015179.
XX
XX 03-JAN-2001; 2001DE-01000127.
XX
XX (HENK) HENKEL KGAA.
XX
XX Petersohn D, Conradt M, Hofmann K;
PI
XX WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
XX Claim 24; Page 312; 1345pp; German.
XX
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
XX Sequence 11 BP; 5 A; 2 C; 3 G; 1 T; 0 U; 0 Other;
SQ
Query Match 28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CTACGTGT 14
 Db 11 CTACGTGT 4

RESULT 545
 ABV65919
 ID ABV65919 standard; cDNA; 11 BP.
 XX AC ABV65919;
 XX DT 21-OCT-2002 (first entry)
 XX DE Human skin EST 3705.
 XX KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX OS Homo sapiens.
 XX PN WO200253774-A2.
 XX PD 11-JUL-2002.
 XX PF 20-DEC-2001; 2001WO-EP015179.
 XX PR 03-JAN-2001; 2001DE-01000127.
 XX PA (HENK) HENKEL KGAA.
 XX PI Petersohn D, Conradt M, Hofmann K;
 XX DR WPI; 2002-590638/63.
 XX PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX PS Disclosure; Page 128; 1345pp; German.
 XX CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX SQ Sequence 11 BP; 1 A; 2 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.7e-02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 GGGAGTCC 25
 Db 4 GGGAGTCC 11

RESULT 546
 ABV63398
 ID ABV63398 standard; cDNA; 11 BP.
 XX AC ABV63398;
 XX DT 21-OCT-2002 (first entry)

XX Human skin EST 1184.
 DE Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX OS Homo sapiens.
 XX PN WO200253774-A2.
 XX PD 11-JUL-2002.
 XX PF 20-DEC-2001; 2001WO-EP015179.
 XX PR 03-JAN-2001; 2001DE-01000127.
 XX PA (HENK) HENKEL KGAA.
 XX PI Petersohn D, Conradt M, Hofmann K;
 XX DR WPI; 2002-590638/63.
 XX PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX PS Disclosure; Page 57; 1345pp; German.
 XX CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX SQ Sequence 11 BP; 3 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.7e-02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 TGTACAGG 19
 Db 4 TGTACAGG 11

RESULT 547
 ABV64393/c
 ID ABV64393 standard; cDNA; 11 BP.
 XX AC ABV64393;
 XX DT 21-OCT-2002 (first entry)
 XX DE Human skin EST 2179.
 XX KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX OS Homo sapiens.
 XX PN WO200253774-A2.
 XX PD 11-JUL-2002.

PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
XX WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
XX Disclosure; Page 85; 1345pp; German.
XX
XX The invention relates to in vitro identification (M1) of genes expressed
XX in the skin of humans or animals by subjecting a mixture of genetically
XX encoded factors from skin, to serial analysis of gene expression (SAGE)
XX so as to identify skin-expressed genes and quantify their expression.
XX (M1) is useful for identifying genes involved in skin homeostasis; to
XX determine skin homeostasis and to test agent (A) that maintains or
XX promotes skin homeostasis or that can be used for treating skin
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX skin. The present sequence is that of a human expressed sequence tag
XX (EST) of the invention
XX
SQ Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 GAGTCCAG 27
DB 11 GAGTCCAG 4
|||||
RESULT 548
ABV64443/c
ID ABV64443 standard; cDNA; 11 BP.
XX
AC ABV64443;
XX
XX 21-OCT-2002 (first entry)
XX
XX Human skin EST 2229.
XX
XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
XX immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
XX
XX WO200253774-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-EP015179.
XX
XX 03-JAN-2001; 2001DE-01000127.
XX
XX (HENK) HENKEL KGAA.
XX
XX Petersohn D, Conradt M, Hofmann K;
XX
XX WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
PT

XX Disclosure; Page 87; 1345pp; German.
PS
XX
XX The invention relates to in vitro identification (M1) of genes expressed
XX in the skin of humans or animals by subjecting a mixture of genetically
XX encoded factors from skin, to serial analysis of gene expression (SAGE)
XX so as to identify skin-expressed genes and quantify their expression.
XX (M1) is useful for identifying genes involved in skin homeostasis; to
XX determine skin homeostasis and to test agent (A) that maintains or
XX promotes skin homeostasis or that can be used for treating skin
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX skin. The present sequence is that of a human expressed sequence tag
XX (EST) of the invention
XX
SQ Sequence 11 BP; 5 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTACGTGT 14
DB 11 CTACGTGT 4
|||||
RESULT 549
ABV72049
ID ABV72049 standard; cDNA; 11 BP.
XX
XX ABV72049;
XX
XX 21-OCT-2002 (first entry)
XX
XX Human skin EST 9835.
XX
XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
XX immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
XX
XX WO200253774-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-EP015179.
XX
XX 03-JAN-2001; 2001DE-01000127.
XX
XX (HENK) HENKEL KGAA.
XX
XX Petersohn D, Conradt M, Hofmann K;
XX
XX WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
XX Claim 24; Page 319; 1345pp; German.
XX
XX The invention relates to in vitro identification (M1) of genes expressed
XX in the skin of humans or animals by subjecting a mixture of genetically
XX encoded factors from skin, to serial analysis of gene expression (SAGE)
XX so as to identify skin-expressed genes and quantify their expression.
XX (M1) is useful for identifying genes involved in skin homeostasis; to
XX determine skin homeostasis and to test agent (A) that maintains or
XX promotes skin homeostasis or that can be used for treating skin
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX skin. The present sequence is that of a human expressed sequence tag
XX (EST) of the invention
XX

CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX Sequence 11 BP; 3 A; 2 C; 4 G; 2 T; 0 U; 0 Other;
SQ

Query Match 28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 GGAGTCCA 26
Db 3 GGAGTCCA 10

RESULT 550
ABV69736
ID ABV69736 standard; cDNA; 11 BP.
XX
AC ABV69736;
XX
XX 21-OCT-2002 (first entry)
XX Human skin EST 7522.
XX
XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
XX WO200253774-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-EP015179.
XX
XX 03-JAN-2001; 2001DE-01000127.
XX (HENK) HENKEL KGAA.
XX
XX Petersohn D, Conradt M, Hofmann K;
PI
XX
XX WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
XX Claim 24; Page 237; 1345pp; German.
XX
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE).
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
XX Sequence 11 BP; 4 A; 2 C; 5 G; 0 T; 0 U; 0 Other;
SQ

Query Match 28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 ACAGGGAG 22
Db 2 ACAGGGAG 9

RESULT 551
ABV6268
ID ABV6268 standard; cDNA; 11 BP.
XX
AC ABV6268;
XX
XX 21-OCT-2002 (first entry)
XX Human skin EST 4054.
XX
XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
XX WO200253774-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-EP015179.
XX
XX 03-JAN-2001; 2001DE-01000127.
XX (HENK) HENKEL KGAA.
XX
XX Petersohn D, Conradt M, Hofmann K;
PI
XX
XX WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
XX Disclosure; Page 137; 1345pp; German.
XX
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE).
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
XX Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
SQ

Query Match 28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred.No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGCGCCTA 9
Db 3 GGCGCCTA 10

RESULT 552
ABV68998/C
ID ABV68998 standard; cDNA; 11 BP.
XX
AC ABV68998;
XX
XX 21-OCT-2002 (first entry)
XX Human skin EST 6784.
XX
XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;

KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX Homo sapiens.
XX WO200253774-A2.
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-EP015179.
XX
XX 03-JAN-2001; 2001DB-01000127.
XX
XX (HENK) HENKEL KGAA.
XX
XX Petersohn D, Conradt M, Hofmann K;
XX WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining
XX homeostasis and identifying cosmetic or pharmaceutical agents against
XX e.g. skin cancer.
XX
XX Disclosure; Page 213; 1345pp; German.
XX
XX The invention relates to in vitro identification (M1) of genes expressed
XX in the skin of humans or animals by subjecting a mixture of genetically
XX encoded factors from skin, to serial analysis of gene expression (SAGE)
XX so as to identify skin-expressed genes and quantify their expression.
XX (M1) is useful for identifying genes involved in skin homeostasis; to
XX determine skin homeostasis and to test agent (A) that maintains or
XX promotes skin homeostasis or that can be used for treating skin
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX skin. The present sequence is that of a human expressed sequence tag
XX (EST) of the invention
XX
SQ Sequence 11 BP; 1 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 GAGTCCAG 27
Db 9 GAGTCCAG 2
|||||||
|

RESULT 553
ABL91942
ID ABL91942 standard; cDNA; 11 BP.
XX
XX ABL91942;
AC
XX
XX 30-MAY-2002 (first entry)
DT
XX
XX Human Pan-Endothelial Marker SEQ ID NO 40.
DE
XX
XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
XX normal endothelial marker; pan-endothelial marker; immunostimulant;
XX antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
XX polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
XX psoriasis; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200210217-A2.
PN
XX
XX 07-FEB-2002.
PD
XX
XX 01-AUG-2001; 2001WO-US024031.
PF
XX
XX 02-AUG-2000; 2000US-0222599P.
PR

PR 11-AUG-2000; 2000US-0224360P.
PR 11-APR-2001; 2001US-0282850P.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX St Croix B, Kinzler KW, Vogelstein B;
XX WPI; 2002-291856/33.
XX
XX An isolated molecule comprising an antibody variable region which
XX specifically binds to an extracellular domain of a tumor endothelial
XX marker (TEM) protein, useful for inhibiting tumor growth.
XX
XX Example 4; Page 325; 331pp; English.
XX
XX The invention relates to an isolated molecule comprising an antibody
XX variable region which specifically binds to an extracellular domain of a
XX tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
XX ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
XX proteins have cytostatic, immunostimulant and antiangiogenic activity.
XX They are useful for inhibiting tumour growth, neoangiogenesis in subjects
XX bearing a vascularised tumour, polycystic kidney disease, diabetic
XX retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
XX genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
XX are disclosed, as are marker oligonucleotide sequences: tumour
XX endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
XX endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
XX (PEM) ABL91903-ABL91995. The present sequence is that of an
XX oligonucleotide marker useful to the invention
XX
SQ Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGCCTTAC 10
Db 1 GGCCTTAC 8
|||||||
|

RESULT 554
ABK68760/C
ID ABK68760 standard; DNA; 11 BP.
XX
XX ABK68760;
AC
XX
XX 02-JUL-2002 (first entry)
DT
XX
XX Oligonucleotide #6 for detecting SNP in 5'-region of human CYP3A4 gene.
DE
XX
XX Human; single nucleotide polymorphism; SNP; cytochrome p450; CYP; CYP3A4;
XX ss.
XX
XX Homo sapiens.
OS
XX
XX WO200218641-A2.
PN
XX
XX 07-MAR-2002.
PD
XX
XX 30-AUG-2001; 2001WO-IB001580.
PF
XX
XX 30-AUG-2000; 2000GB-00021286.
PR
XX
XX (GEMI-) GEMINI GENOMICS PLC.
PA
XX
XX Risinger C, Andersson MK, Lewander T, Olafsson E;
XX WPI; 2002-351712/38.
XX
XX Novel primer pairs and sequence determination oligonucleotides useful for
XX amplifying and detecting novel single nucleotide polymorphisms in the 5'
XX flanking regions of cytochrome p450 (CYP)3A4 and CYP2C9 genes
XX

PT respectively.
XX
XX Claim 4; Page 17; 47pp; English.
XX
CC The present invention relates to PCR primer pairs for amplifying and
CC sequence determination oligonucleotides for detecting single nucleotide
CC polymorphisms (SNPs) in the 5'-flanking regions of human cytochrome p450
CC (CYP) genes encoding CYP3A4 or CYP2C9. The SNPs correspond to position
CC 461 of a defined 1345 base pair sequence for CYP3A4 or position 957,
CC 1049, 1164, 1526, 1661 and 1662 of a 2438 base pair sequence for CYP2C9.
CC The PCR primers are useful for amplifying the CYP sequences and the
CC oligonucleotides are useful for detecting SNPs in the 5'-flanking regions
CC of the CYP3A4 or CYP2C9 genes. ABK68755-ABK68761 represent
CC oligonucleotides for detecting the polymorphism in the 5'-flanking region
CC of the human CYP3A4 gene
XX
XX Sequence 11 BP; 3 A; 4 C; 2 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 28.6%; Score 8; DB 1; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0;
XX
Qy 11 GTGTACAG 18
Db 9 GTGTACAG 2

XX
XX RESULT 555
XX ABK68759
XX ID ABK68759 standard; DNA; 11 BP.
XX AC ABK68759;
XX
XX 02-JUL-2002 (first entry)
XX
XX Oligonucleotide #5 for detecting SNP in 5'-region of human CYP3A4 gene.
XX
XX Human; single nucleotide polymorphism; SNP; cytochrome p450; CYP; CYP3A4;
XX ss.
XX Homo sapiens.
XX
XX WO200218641-A2.
XX
XX 07-MAR-2002.
XX
XX 30-AUG-2001; 2001WO-IB001580.
XX
XX 30-AUG-2000; 2000GB-00021286.
XX
XX (GEMI-) GEMINI GENOMICS PLC.
XX
XX Risinger C, Andersson MK, Lewander T, Olaisson E;
XX WPI; 2002-351712/38.
XX
XX Novel primer pairs and sequence determination oligonucleotides useful for
XX amplifying and detecting novel single nucleotide polymorphisms in the 5'
XX flanking regions of cytochrome p450 (CYP)3A4 and CYP2C9 genes
XX respectively.
XX
XX Claim 4; Page 17; 47pp; English.
XX
XX The present invention relates to PCR primer pairs for amplifying and
XX sequence determination oligonucleotides for detecting single nucleotide
XX polymorphisms (SNPs) in the 5'-flanking regions of human cytochrome p450
XX (CYP) genes encoding CYP3A4 or CYP2C9. The SNPs correspond to position
XX 461 of a defined 1345 base pair sequence for CYP3A4 or position 957,
XX 1049, 1164, 1526, 1661 and 1662 of a 2438 base pair sequence for CYP2C9.
XX The PCR primers are useful for amplifying the CYP sequences and the
XX oligonucleotides are useful for detecting SNPs in the 5'-flanking regions
XX of the CYP3A4 or CYP2C9 genes. ABK68755-ABK68761 represent
XX oligonucleotides for detecting the polymorphism in the 5'-flanking region

CC of the human CYP3A4 gene
XX
XX Sequence 11 BP; 2 A; 2 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 28.6%; Score 8; DB 1; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0;
XX
Qy 11 GTGTACAG 18
Db 3 GTGTACAG 10

XX
XX RESULT 556
XX ABL51577/c
XX ID ABL51577 standard; DNA; 11 BP.
XX AC ABL51577;
XX
XX 03-JUL-2002 (first entry)
XX
XX Transferrin receptor gene related oligonucleotide fragment #7.
XX
XX Polymorphism; single nucleotide polymorphism; SNP; identification;
XX detection; hybridisation; genotyping; transferrin receptor; human; ss.
XX Homo sapiens.
XX Synthetic.
XX
XX WO200221098-A2.
XX
XX 14-MAR-2002.
XX
XX 04-SEP-2001; 2001WO-US027446.
XX
XX 05-SEP-2000; 2000US-00655104.
XX
XX (VARI-) VARIAGENICS INC.
XX
XX Stanton VP, Wolfe JL, Kawate T, Verdine GL;
XX WPI; 2002-362259/39.
XX
XX Detecting polymorphism in a polynucleotide (N) comprises hybridizing an
XX oligonucleotide with a variant (N) having modified nucleotides
XX incorporated at each point of suspected polymorphism occurrence.
XX
XX Example 4; Fig 29b; 245pp; English.
XX
XX The present invention describes a method for detecting a polymorphism (P)
XX in polynucleotide (N). The method comprises: (1) hybridising
XX oligonucleotides with fragments of (N) segments which contain a
XX polymorphism, and have modified nucleotides that are incorporated at each
XX point of occurrence of suspected (P) during amplification; and (2)
XX analysing the hybridising fragments for an incorporated detectable label
XX identifying the susceptible polymorphism. The method is used for
XX detecting polymorphisms (e.g. a single nucleotide polymorphism (SNP), a
XX deletion or an insertion) in (N). The method is useful for developing
XX diagnostic and prognostic tools for detecting a predisposition of certain
XX disease and disorders. The method is useful for detecting variance in DNA
XX sequencing, and has applications in genotyping. The present sequence
XX represents a transferrin receptor gene related oligonucleotide sequence,
XX which is used in an example from the present invention
XX
XX Sequence 11 BP; 0 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 28.6%; Score 8; DB 1; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0;
XX
Qy 15 ACAGGGAG 22
Db 11 ACAGGGAG 4

RESULT 557
ABX71867
ID ABX71867 standard; DNA; 11 BP.
AC ABX71867;
XX
DT 12-MAR-2003 (first entry)
XX
DE DNA tag used to identify human gene encoding PEM 40.
XX
KW Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;
KW Tumour endothelial marker; normal endothelial marker; PEM;
KW Pan-endothelial marker; polycystic kidney disease; psoriasis;
KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
KW neovascularization; immune response; cytostatic; antidiabetic;
KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic; ds.
XX
OS Homo sapiens.
XX
PN WO200283874-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US008253.
XX
PR 11-APR-2001; 2001US-0282850P.
PR 06-FEB-2002; 2002US-0354262P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;
XX WPI; 2003-093016/08.
XX
PT New purified human transmembrane protein, designated as tumor endothelial
PT marker (TEM) 3, useful for detecting, diagnosing or treating tumors,
PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
PT psoriasis.
XX
PS Disclosure; Page 93; 374pp; English.
XX
CC The present invention relates to a novel method for the isolation of
CC endothelial cells (ECs), and the identification of genes expressed in
CC normal and tumour ECs. Tumour endothelial marker (TEM), normal
CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are
CC identified in human ECs. The human EC marker proteins and the
CC polynucleotide sequences encoding them are useful for detecting,
CC diagnosing or treating tumours as well as polycystic kidney disease,
CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also
CC useful for inhibiting neoangiogenesis or tumour angiogenesis, for
CC inducing an immune response to tumour endothelial cells in a patient, or
CC for identifying candidate drugs for treating tumours. ABX71828-ABX71999
CC represent DNA tags for human PEM, TEM or NEM genes
XX
SQ Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 28.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GGCCCTAC 10
DB 1 GGCCCTAC 8
RESULT 558
AA79373
ID AAX79373 standard; DNA; 12 BP.
XX
AC AAX79373;
XX

DT 17-AUG-1999 (first entry)
XX
DE HLA-DR typing probe L74.
XX
KW Tissue typing; human leukocyte antigen; HLA; MHC; donor; allele; PCR;
KW major histocompatibility complex; bone marrow transplant; primer;
KW amplification; polymerase chain reaction; probe; polymorphism;
KW sequence-specific oligonucleotide probe hybridisation; ss.
XX
OS Synthetic.
XX
PN US5468611-A.
XX
PD 21-NOV-1995.
XX
PF 08-APR-1993; 93US-00045530.
XX
PR 27-JUN-1990; 90US-00544218.
XX
PA (BLOO-) BLOOD CENT RES FOUND INC.
XX
PI Gorski JA, Baxter-Lowe LA;
XX WPI; 1996-010091/01.
XX
PT Improved method for HLA typing - by DNA amplification and sequence-
PT specific oligonucleotide hybridisation, used to select bone marrow
PT donors.
XX
PS Disclosure; Col 19-20; 20pp; English.
XX
CC A novel method of typing the human leukocyte antigen (HLA) of the major
CC histocompatibility complex (MHC), esp. for typing donors for bone marrow
CC transplants, involves determining if the donor tissue HLA-DR alleles are
CC selected from the gp.: HLA-DRW52C, DR12a.b, DR3a.n, DR5a-e, DRNew1, DR6a,
CC DR8a-d, DRW53a-c, DR4a-f, DR7, DR9, DR2a-c B3, DR2a-d B1, DR10 and DR1a-
CC c. The method uses PCR to amplify these regions followed by sequence-
CC specific oligonucleotide probe hybridisation (SSOPH) using the probes
CC AAX79365-X79429. SSOPH allows detection of polymorphisms that predict
CC differences at a single amino acid level thus reducing errors and
CC improving the chance of successfully matching tissues
XX
SQ Sequence 12 BP; 1 A; 4 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGGCCCT 8
DB 4 CGGGCCCT 11
RESULT 559
AA741818/c
ID AAT41818 standard; DNA; 12 BP.
XX
AC AAT41818;
XX
DT 25-MAR-2003 (revised)
DT 18-DEC-1996 (first entry)
XX
DE HLA allele, HLA-DRB1*08, *12 and *1404 resolution probe, L74.
XX
KW Human leukocyte antigen; HLA; allele; HLA-DR*08; HLA-DR*12; locus B1;
KW polymorphism; amplify; conserved region; detection; probe;
KW tissue matching; identifying disease susceptibility; ss.
XX
OS Synthetic.
XX
PN US5545526-A.
XX
PD 13-AUG-1996.

XX PF 01-MAR-1993; 93US-00025039.
 XX PR 27-JUN-1990; 90US-00544218.
 XX PA (BLOO-) BLOOD CENT RES FOUND INC.
 XX PI Baxter-Lowe LA;
 XX XX WPI; 1996-383664/38.
 XX PT Human leukocyte antigen typing of tissue samples - using allele-specific
 XX PT amplification to distinguish allele pairs.
 XX PS Example 1; Col 19; 24pp; English.
 XX XX The sequences given in AAT1811-20 represent probes which were used to
 CC resolve the human leukocyte antigen (HLA) DRB1 alleles, DRB1*08, *12 and
 CC *1404. This probe sequence hybridises to the Leu74 coding region found in
 CC alleles *0801, *0802, *0803 and 0804. These probes may be used in the
 CC method of invention which concerns HLA typing of a sample for an unknown
 CC pair of alleles. The pair of alleles comprises one of two known types
 CC which have the same overall set of polymorphisms but have a different
 CC distribution of polymorphisms between their two alleles. The method
 CC comprises selectively amplifying the DNA of just one allele of the
 CC unknown pair and analysing the amplified DNA to determine which
 CC polymorphisms are present in that allele, and therefore assigning the
 CC unknown pair to the known type having that allele. The method comprises
 CC three test stages. The first stage is to establish the number of alleles
 CC present in each sample. Primers corresponding to fairly well conserved
 CC regions of a locus will increase the likelihood that unknown alleles will
 CC be amplified and potentially detected by hybridisation with a probe. In
 CC the second stage, the group or basic type identified determines which set
 CC of allele specific primers will be used. The first of the two primers
 CC comprises an opt. labeled sequence common to each allele of the group
 CC identified in the first stage but different from other groups identified
 CC in stage one. The second primer may be a mixture of different labeled
 CC primers, complementary to two or more sequences within the group, or the
 CC amplification may be performed with only one second primer to detect the
 CC presence of a single group of alleles. In the third stage the specific
 CC allele is determined. This may be done by amplification or hybridisation
 CC using a radiolabelled probe. The method may be used for tissue matching,
 CC identifying disease susceptibility, etc. The method of the invention esp.
 CC distinguishes between DQB1*0304/DQB1*0302 and DQB1*0301/DQB1*0302.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX SQ Sequence 12 BP; 1 A; 6 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 28.6%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGGGCCCT 8
 Db |||||
 9 CGGGCCCT 2
 RESULT 560
 AAV16569
 ID AAV16569 standard; DNA; 12 BP.
 AC AAV16569;
 XX 12-JUN-1998 (first entry)
 DT Probe L74 used to identify HLA-DR sequences.
 DE DR region; major histocompatibility complex; HLA-DR; HLA-typing;
 XX HLA-DR Beta consensus sequence; allelic polymorphism;
 KW HLA-DR beta-allelic polymorphism; probe; bone marrow; transplant; ss.
 XX Synthetic.
 OS Homo sapiens.

XX PN US5702885-A.
 XX PD 30-DEC-1997.
 XX PF 08-APR-1993; 93US-00057957.
 XX PR 27-JUN-1990; 90US-00544218.
 XX PA (BLOO-) BLOOD CENT RES FOUND INC.
 XX PI Gorski JA, Baxter-Lowe LA;
 XX XX WPI; 1998-076408/07.
 XX PT Oligo:nucleotide probes and primers and methods for HLA typing -
 XX PT particularly for tissue typing for bone marrow transplants.
 XX PS Disclosure; Col 19; 20pp; English.
 XX XX Probes AAV16561-624 are used to identify differences in the DR region of
 CC human major histocompatibility complex (HLA-DR). The specification
 CC describes a method for HLA-typing, which includes an oligonucleotide
 CC probe which undergoes sequence-specific hybridisation with an HLA-DR beta
 CC consensus sequence at positions 61-84. The probe contains a labelling
 CC substance other than a nucleotide sequence, which facilitates detection
 CC of the probe. The HLA sequence of a subject is PCR amplified, and a probe
 CC that recognises an allelic polymorphism at a selected HLA locus is
 CC contacted with the amplified product. This first probe recognises a HLA-
 CC DR beta-allelic polymorphism. A second (different) probe is brought into
 CC contact with a second sample of the amplified DNA in a separate reaction,
 CC and hybridisation detected. The probes and primers are used for HLA
 CC typing, e.g. for tissue, especially bone marrow, transplants
 XX SQ Sequence 12 BP; 1 A; 4 C; 6 G; 1 T; 0 U; 0 Other;
 Query Match 28.6%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGGGCCCT 8
 Db |||||
 4 CGGGCCCT 11
 RESULT 561
 ABH93621/C
 ID ABH93621 standard; DNA; 12 BP.
 XX AC ABH93621;
 XX 22-FEB-2002 (first entry)
 DT Oligonucleotide primer SEQ ID NO 293614 for detecting SNP TSC0015707.
 XX DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPITG-) EPITGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;

DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX
 PS Claim 1; SEQ ID NO 293614; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 6 A; 3 C; 1 G; 2 T; 0 U; 0 Other;
 Query Match 28.6%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 TACGTGTA 15
 Db 12 TACGTGTA 5
 RESULT 562
 ID ABI06748/c
 XX ABI06748 standard; DNA; 12 BP.
 AC ABI06748;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 306721 for detecting SNP TSC0022148.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 OS
 XX
 XX W0200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX
 PS Claim 1; SEQ ID NO 306721; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 4 A; 3 C; 1 G; 4 T; 0 U; 0 Other;
 Query Match 28.6%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 TACGTGTA 15
 Db 8 TACGTGTA 1
 RESULT 563
 ID ABH95544
 XX ABH95544 standard; DNA; 12 BP.
 AC ABH95544;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 295537 for detecting SNP TSC0016628.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 OS
 XX
 XX W0200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX
 PS Claim 1; SEQ ID NO 295537; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 4 A; 4 C; 1 G; 3 T; 0 U; 0 Other;
 Query Match 28.6%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCTACGTT 12
Db 5 CCTACGTT 12
RESULT 564
ABI56358
ID ABI56358 standard; DNA; 12 BP.
AC ABI56358;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 356331 for detecting SNP TSC0050060.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
PN
XX
DT 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 356331; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 1 C; 3 G; 4 T; 0 U; 0 Other;
XX
Query Match 28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 TACGTGTA 15
Db 1 TACGTGTA 8
RESULT 565
ABH70251
ID ABH70251 standard; DNA; 12 BP.
XX
AC ABH70251;
XX
DT 22-FEB-2002 (first entry)
XX

XX
DE Oligonucleotide primer SEQ ID NO 270228 for detecting SNP TSC0002052.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
PN
XX
DT 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 270228; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 1 C; 3 G; 6 T; 0 U; 0 Other;
XX
Query Match 28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 TACGTGTA 15
Db 2 TACGTGTA 9
RESULT 566
ABH89284
ID ABH89284 standard; DNA; 12 BP.
XX
AC ABH89284;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 289277 for detecting SNP TSC0013867.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
PN
XX
DT 18-OCT-2001.
XX

PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 289277; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 1 C; 4 G; 3 T; 0 U; 0 Other;
SQ
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 TACGTGTA 15
DB 3 TACGTGTA 10
|||||||
RESULT 567
ABH92486/c
ID ABH92486 standard; DNA; 12 BP.
XX
XX ABH92486;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 292479 for detecting SNP TSC0015230.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
DE designed to detect single-nucleotide polymorphisms and cytosine
DE methylation status.
XX
XX Claim 1; SEQ ID NO 289277; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 4 A; 1 C; 4 G; 3 T; 0 U; 0 Other;
SQ

XX Claim 1; SEQ ID NO 292479; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 1 A; 2 C; 5 G; 4 T; 0 U; 0 Other;
SQ
XX Query Match 28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GCCCTACG 11
DB 10 GCCCTACG 3
|||||||
RESULT 568
AB113410
ID AB113410 standard; DNA; 12 BP.
XX
XX AB113410;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 313383 for detecting SNP TSC0025713.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 313383; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 1 A; 2 C; 5 G; 4 T; 0 U; 0 Other;
SQ

CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCTACGT 12
|||||||
Db 5 CCTACGT 12

RESULT 569

AB162488
ID AB162488 standard; DNA; 12 BP.

XX
AC AB162488;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 362461 for detecting SNP TSC0053239.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 362461; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 4 A; 1 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TACGTGTA 15
|||||||
Db 4 TACGTGTA 11

RESULT 570

AB113984
ID AB113984 standard; DNA; 12 BP.

XX
AC AB113984;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 313957 for detecting SNP TSC0026047.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 313957; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 3 A; 1 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TACGTGTA 15
|||||||
Db 2 TACGTGTA 9

RESULT 571

ABH95542/c
ID ABH95542 standard; DNA; 12 BP.

XX
AC ABH95542;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 295535 for detecting SNP TSC0016627.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPITG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 295535; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 1 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 CCTACGT 12
DB 8 CCTACGT 1
RESULT 572
ABH76707
ID ABH76707 standard; DNA; 12 BP.
XX
XX ABH76707;
XX
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 276700 for detecting SNP TSC0004266.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPITG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 276700; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 2 A; 1 C; 3 G; 5 T; 0 U; 0 Other;
Query Match 28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 8 TACGTGTA 15
DB 3 TACGTGTA 10
RESULT 573
ABI76102/c
ID ABI76102 standard; DNA; 12 BP.
XX
XX ABI76102;
XX
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 376075 for detecting SNP TSC0061603.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPITG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 376075; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCTACGCT 12
Db 10 CCTACGCT 3

RESULT 574
ABH81705
ID ABH81705 standard; DNA; 12 BP.
AC ABH81705;
XX
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer 65Q ID NO 281698 for detecting SNP TSC0010001.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 281698; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 1 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TACGTGTA 15
Db 5 TACGTGTA 12

RESULT 575
ABH85829/c
ID ABH85829 standard; DNA; 12 BP.
XX
XX ABH85829;
XX
XX 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 285822 for detecting SNP TSC0012462.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 285822; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 6 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TACGTGTA 15
Db 10 TACGTGTA 3

RESULT 576
ABH86354
ID ABH86354 standard; DNA; 12 BP.
XX

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 297053; 29pp + Sequence Listing; German.
 CC
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 3 A; 1 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 28.6%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 CCTACGT 12
 Db 10 CCTACGT 3
 RESULT 579
 ABI16213
 ID ABI16213 standard; DNA; 12 BP.
 AC
 AC ABI16213;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 316186 for detecting SNP TSC0027326.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 316186; 29pp + Sequence Listing; German.
 CC
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 4 A; 1 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 28.6%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 17 AGGAGTC 24
 Db 5 AGGAGTC 12
 RESULT 580
 ABI56360
 ID ABI56360 standard; DNA; 12 BP.
 XX
 AC ABI56360;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 356333 for detecting SNP TSC0050060.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 356333; 29pp + Sequence Listing; German.
 CC
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 4 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 28.6%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 8 TACGTGTA 15

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Db      1 TACGTGTA 8
|||||||
RESULT 581
ABI28945/C
ID ABI28945 standard; DNA; 12 BP.
AC      ABI28945;
XX
XX      22-FEB-2002 (first entry)
XX
XX      Oligonucleotide primer SEQ ID NO 328918 for detecting SNP TSC0034654.
DE
XX      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX      Homo sapiens.
OS
XX      WO200177384-A2.
PN
XX      18-OCT-2001.
PD
XX
XX      06-APR-2001; 2001WO-IB000713.
PF
XX      07-APR-2000; 2000DE-01019173.
PR
XX      (EPIC-) EPIGENOMICS AG.
XX
XX      Olek A, Piepenbrock C, Berlin K;
PI
XX      WPI; 2001-657177/75.
DR
XX
XX      Set of oligonucleotides, useful for diagnosis and cell typing, is
PT      designed to detect single-nucleotide polymorphisms and cytosine
PT      methylation status.
XX
XX      Claim 1; SEQ ID NO 328918; 29pp + Sequence Listing; German.
XX
XX      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC99989, ABP0010-ABF99989, ABH0010-ABH99989 and ABI0010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
XX      Sequence 12 BP; 2 A; 6 C; 1 G; 3 T; 0 U; 0 Other;
SQ
XX
XX      Query Match      28.6%; Score 8; DB 1; Length 12;
XX      Best Local Similarity 100.0%; Pred. No. 3.1e+02;
XX      Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy      17 AGGGAGTC 24
Db      11 AGGGAGTC 4
|||||||
RESULT 582
ABI10703/C
ID ABI10703 standard; DNA; 12 BP.
AC      ABI10703;
XX
XX      22-FEB-2002 (first entry)
XX
XX      Oligonucleotide primer SEQ ID NO 310676 for detecting SNP TSC0024049.
DE

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```

XX      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX      Homo sapiens.
OS
XX      WO200177384-A2.
PN
XX      18-OCT-2001.
PD
XX
XX      06-APR-2001; 2001WO-IB000713.
PF
XX      07-APR-2000; 2000DE-01019173.
PR
XX      (EPIC-) EPIGENOMICS AG.
XX
XX      Olek A, Piepenbrock C, Berlin K;
PI
XX      WPI; 2001-657177/75.
DR
XX
XX      Set of oligonucleotides, useful for diagnosis and cell typing, is
PT      designed to detect single-nucleotide polymorphisms and cytosine
PT      methylation status.
XX
XX      Claim 1; SEQ ID NO 310676; 29pp + Sequence Listing; German.
XX
XX      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC99989, ABP0010-ABF99989, ABH0010-ABH99989 and ABI0010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
XX      Sequence 12 BP; 4 A; 4 C; 1 G; 3 T; 0 U; 0 Other;
SQ
XX
XX      Query Match      28.6%; Score 8; DB 1; Length 12;
XX      Best Local Similarity 100.0%; Pred. No. 3.1e+02;
XX      Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy      8 TACGTGTA 15
Db      11 TACGTGTA 4
|||||||
RESULT 583
ABI75403/C
ID ABI75403 standard; DNA; 12 BP.
AC      ABI75403;
XX
XX      22-FEB-2002 (first entry)
XX
XX      Oligonucleotide primer SEQ ID NO 375376 for detecting SNP TSC0061224.
DE
XX      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX      Homo sapiens.
OS
XX      WO200177384-A2.
PN
XX      18-OCT-2001.
PD
XX
XX      06-APR-2001; 2001WO-IB000713.
PF
XX

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PR 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
PA Olek A, Piepenbrock C, Berlin K;
PI WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 375376; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 5 A; 1 C; 4 G; 2 T; 0 U; 0 Other;
SQ
XX
XX Query Match 28.6%; Score 8; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 3.1e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 5 CCCTACGT 12
XX
XX Db 9 CCCTACGT 2
XX
XX RESULT 584
XX ABI63259
XX ID ABI63259 standard; DNA; 12 BP.
XX AC ABI63259;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 363232 for detecting SNP TSC0053719.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 363232; 29pp + Sequence Listing; German.

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XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 2 A; 1 C; 3 G; 6 T; 0 U; 0 Other;
SQ
XX
XX Query Match 28.6%; Score 8; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 3.1e+02;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 8 TACGTGTA 15
XX
XX Db 3 TACGTGTA 10
XX
XX RESULT 585
XX ABH73580
XX ID ABH73580 standard; DNA; 12 BP.
XX AC ABH73580;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 273565 for detecting SNP TSC0003234.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 273565; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX

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XX SQ Sequence 12 BP; 2 A; 1 C; 4 G; 5 T; 0 U; 0 Other;
Query Match      28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred.No. 3.1e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 TACGTGTA 15
DB      3 TACGTGTA 10
|||||||
RESULT 586
ABI5650/c
ID ABI56650 standard; DNA; 12 BP.
XX AC ABI56650;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 356623 for detecting SNP TSC0050224.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 356623; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX PS Sequence 12 BP; 6 A; 3 C; 1 G; 2 T; 0 U; 0 Other;
Query Match      28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred.No. 3.1e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 TACGTGTA 15
DB      11 TACGTGTA 4
|||||||
RESULT 587

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ABI59399/c
ID ABI59399 standard; DNA; 12 BP.
XX AC ABI59399;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 359372 for detecting SNP TSC0051583.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 359372; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX PS Sequence 12 BP; 6 A; 2 C; 1 G; 3 T; 0 U; 0 Other;
Query Match      28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred.No. 3.1e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 TACGTGTA 15
DB      9 TACGTGTA 2
|||||||
RESULT 588
AAF92629
ID AAF92629 standard; DNA; 12 BP.
XX AC AAF92629;
XX DT 16-MAY-2001 (first entry)
XX DE HLA-DR typing probe #9.
XX KW Human; leukocyte antigen; HLA; typing; sequence specific probe; SSOPH;
XX KW ss.
XX OS Homo sapiens.

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XX US6194147-B1.
 XX
 XX PD 27-FEB-2001.
 XX
 XX PF 30-DEC-1997; 97US-0000805.
 XX
 XX PR 27-JUN-1990; 90US-00544218.
 XX PR 08-APR-1993; 93US-00057957.
 XX
 XX PA (BLOO-) BLOOD CENT RES FOUND INC.
 XX
 XX PI Baxter-Lowe LA, Gorski JA;
 XX
 XX DR WPI; 2001-217923/22.
 XX
 XX PT Human leukocyte antigen typing by amplifying a sample followed by
 PT sequence specific oligonucleotide hybridization with labeled
 PT oligonucleotide probes that hybridize with a series of known control DNA
 PT sequences.
 XX
 XX PS Disclosure; Col 11-14; 16pp; English.
 XX
 XX CC The present invention relates to human leukocyte antigen (HLA) typing.
 CC The method involves detecting polymorphic residues by sequence specific
 CC oligonucleotide probe hybridization (SSOPH) with labeled oligonucleotide
 CC probes
 XX
 XX SQ Sequence 12 BP; 1 A; 4 C; 6 G; 1 T; 0 U; 0 Other;
 Query Match 28.6%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CGGGCCCT 8
 DB 4 CGGGCCCT 11
 RESULT 589
 ID AAF92695 standard; DNA; 12 BP.
 XX
 XX AC AAF92695;
 XX
 XX DT 16-MAY-2001 (first entry)
 XX
 XX DE HLA-DR allele group typing probe #10.
 XX
 XX KW Human; leukocyte antigen; HLA; typing; sequence specific probe; SSOPH;
 KW ss.
 XX
 XX OS Homo sapiens.
 XX
 XX PN US6194147-B1.
 XX
 XX PD 27-FEB-2001.
 XX
 XX PF 30-DEC-1997; 97US-0000805.
 XX
 XX PR 27-JUN-1990; 90US-00544218.
 XX PR 08-APR-1993; 93US-00057957.
 XX
 XX PA (BLOO-) BLOOD CENT RES FOUND INC.
 XX
 XX PI Baxter-Lowe LA, Gorski JA;
 XX
 XX DR WPI; 2001-217923/22.
 XX
 XX PT Human leukocyte antigen typing by amplifying a sample followed by
 PT sequence specific oligonucleotide hybridization with labeled
 PT oligonucleotide probes that hybridize with a series of known control DNA
 PT sequences.

XX Disclosure; Col 11-14; 16pp; English.
 XX
 XX PS The present invention relates to human leukocyte antigen (HLA) typing.
 CC The method involves detecting polymorphic residues by sequence specific
 CC oligonucleotide probe hybridization (SSOPH) with labeled oligonucleotide
 CC probes
 XX
 XX SQ Sequence 12 BP; 1 A; 4 C; 6 G; 1 T; 0 U; 0 Other;
 Query Match 28.6%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CGGGCCCT 8
 DB 4 CGGGCCCT 11
 RESULT 590
 ID ABL42258 standard; DNA; 12 BP.
 XX
 XX AC ABL42258;
 XX
 XX DT 01-JUL-2002 (first entry)
 XX
 XX DE Plant cis-regulatory sequence from barley ABA.
 XX
 XX KW DNA fingerprinting; cancer; agriculture; breeding; PCR; primer;
 KW gene family; ds.
 XX
 XX OS Hordeum sp.
 XX
 XX PN WO200162967-A2.
 XX
 XX PD 30-AUG-2001.
 XX
 XX PF 19-FEB-2001; 2001WO-IL000151.
 XX
 XX PR 22-FEB-2000; 2000IL-00134660.
 XX PR 02-JUL-2000; 2000IL-00137124.
 XX PR 20-AUG-2000; 2000IL-00137959.
 XX
 XX PA (GENE-) GENEVA LTD.
 XX PA (AGRI-) AGRIC RES ORG NEWE YA'AR RES CENTE.
 XX
 XX PI Vidar B, Katzir N;
 XX
 XX DR WPI; 2002-239525/29.
 XX
 XX PT Polymerase chain reaction based method of DNA fingerprinting, useful for
 PT analyzing genes, e.g. for identifying genes involved in cancer formation,
 PT involves using a mix of primers that match the conserved regions of a
 PT gene family.
 XX
 XX PS Example; Page 17; 28pp; English.
 XX
 XX CC The invention relates to a polymerase chain reaction (PCR) based method
 CC of DNA fingerprinting, comprising using primers that match the conserved
 CC regions of a gene family. The method is useful for gene expression
 CC analysis of any cell or tissue, or for the performance of DNA
 CC fingerprinting analysis of the same organism in order that one will
 CC reveal the function of a gene that produced differential product between
 CC genotypes. The method is also useful for identifying PCR reactions that
 CC contain a gene of interest in a gene family reverse transcriptase (RT)-
 CC PCR expression analysis. The method is also useful for identifying genes
 CC that belong to a gene family that might be involved in cancer formation.
 CC The method is particularly useful for comparing genomic sequences. These
 CC are also applicable in agriculture (e.g. to mark useful genes to assist
 CC breeding). The current sequence represents a plant cis-regulatory
 CC sequence. This is used in DNA fingerprinting using primers or a mix of
 CC primers that match the sequence of ubiquitous cis-acting regulatory

CC elements
 XX Sequence 12 BP; 1 A; 4 C; 5 G; 2 T; 0 U; 0 Other;
 SQ Query Match 28.6%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCTACGTG 13
 |||||
 Db 1 CCTACGTG 8

RESULT S91
 ABX10158
 ID ABX10158 standard; cDNA; 12 BP.
 XX
 AC ABX10158;
 XX
 DT 27-JAN-2003 (first entry)
 XX Human TIGR/Mycillin variant cDNA deletion 3' flank #1.
 XX
 KW Human; ss; TIGR; MYOC; Myocilin; Glaucoma; blindness;
 KW trabecular meshwork inducible glucocorticoid responsive protein;
 KW retinal degenerative disease; RDB; retinitis pigmentosa;
 KW macular degeneration; Usher syndrome; cardiovascular disease;
 KW congenital heart disease; myocardial ischaemia; stroke;
 KW acute endocarditis; hypertensive heart disease; arrhythmia;
 KW arteriosclerotic heart disease.
 XX
 OS Homo sapiens.
 XX
 XX WO200282969-A2.
 PN
 PD 24-OCT-2002.
 XX
 XX 11-DEC-2001; 2001WO-US048622.
 XX
 XX 05-APR-2001; 2001US-0281442P.
 PR
 PR 23-JUL-2001; 2001US-0306889P.
 XX
 XX (KONG/) KONG T H.
 XX
 XX Kong TH;
 XX
 XX WPI; 2003-058597/05.
 DR
 XX Determining the presence or the risk of having glaucoma, retinal
 PT degenerative or cardiovascular diseases in a subject, comprises
 PT generating transcriptional or translational profiles based on myocilin
 PT nucleic acids and proteins.
 PT
 PS Disclosure; Fig 4c; 55pp; English.
 XX
 XX The invention relates to determining whether a subject has or is at risk
 CC of developing glaucoma, retinal degenerative disease, or a cardiovascular
 CC disease, comprises generating a transcriptional or translational profile
 CC (i.e. 'fingerprint') in the subject or in a sample obtained from the
 CC subject, based on the expression of the different myocilin (MYOC, also
 CC known as trabecular meshwork inducible glucocorticoid responsive protein,
 CC TIGR) mRNA species or polypeptide forms, where a difference in the
 CC profile relative to that in a normal subject indicates that the subject
 CC has or is at risk of developing the above-mentioned diseases. Also
 CC included are: (1) a method for establishing MYOC genetic population
 CC profile in a population of individuals having glaucoma, retinal
 CC degenerative disease, or a cardiovascular disease; (2) a method for
 CC pharmacogenomically selecting a therapy to administer to an individual
 CC having glaucoma, retinal degenerative disease, or a cardiovascular
 CC disease, comprising determining MYOC genetic profile of an individual and
 CC comparing the individual's MYOC genetic profile to MYOC genetic
 CC population profile, to select a therapy for administration to the
 CC individual; and a kit for determining whether a subject has or is likely

CC to develop glaucoma, retinal degenerative disease, or a cardiovascular
 CC disease, comprising a probe or primer which hybridises to the MYOC
 CC nucleic acid, or an antibody or peptide probe capable of specifically
 CC binding to the novel MYOC polypeptide(s), and instructions for use. The
 CC method is useful for the prognosis and/or diagnosis of glaucoma, retinal
 CC degenerative diseases (RDB) or cardiovascular diseases (e.g. blindness,
 CC retinitis pigmentosa, macular degeneration, Usher syndrome, congenital
 CC heart disease, myocardial ischaemia, stroke, acute endocarditis,
 CC hypertensive heart disease, arrhythmia and arteriosclerotic heart
 CC disease), and in screening assays for the identification of therapeutics
 CC and the evaluation of their effectiveness for treating the above-
 CC mentioned diseases in a subject. The present sequence represents the 3'
 CC flanking sequence surrounding the deletion present in a MYOC cDNA variant
 XX
 SQ Sequence 12 BP; 4 A; 3 C; 3 G; 2 T; 0 U; 0 Other;
 Query Match 28.6%; Score 8; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 GAGTCCAG 27
 |||||
 Db 2 GAGTCCAG 9

RESULT S92
 AAX09580/c
 ID AAX09580 standard; DNA; 15 BP.
 XX
 AC AAX09580;
 XX
 DT 24-MAR-1999 (first entry)
 XX
 XX Human biallelic polymorphic marker upstream primer #460.
 DE
 XX Polymorphism; biallelic; human; forensic; paternity testing; disease;
 KW detection; phenotypic typing; characteristic; infection; hereditary;
 KW autoimmune disease; cancer; inflammation; drug; therapy; medication;
 KW treatment; marker; primer; ss.
 XX
 XX Synthetic.
 OS
 OS Homo sapiens.
 XX
 XX WO9820165-A2.
 PN
 XX 14-MAY-1998.
 PD
 XX 05-NOV-1997; 97WO-US020313.
 PF
 XX 06-NOV-1996; 96US-0030455P.
 PR
 XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
 PA
 XX Lander ES, Wang D, Hudson T;
 PI
 XX WPI; 1998-286974/25.
 DR
 XX New isolated nucleic acid segments from the human genome - used for
 PT determining polymorphic forms for use in e.g. forensics, paternity
 PT testing or phenotypic typing for disease.
 PT
 XX Claim 15; Page 207; 310pp; English.
 PS
 XX AAX09121-X10268 are allele-specific oligonucleotide primers used in the
 CC isolation of various biallelic polymorphic markers found in the human
 CC genome (represented in AAX10269-X12937). These primers can be used in a
 CC method for determining polymorphic forms in an individual for use in e.g.
 CC forensics, paternity testing or for phenotypic typing for diseases such
 CC as egamaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
 CC dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial
 CC hypercholesterolemia, polycystic kidney disease, hereditary
 CC spherocytosis, von Willebrand's disease, tuberosus sclerosis, hereditary
 CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos

RESULT 595
 ABI23374/c
 ID ABI23374 standard; DNA; 12 BP.
 XX
 AC ABI23374;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 323347 for detecting SNP TSC0031342.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 323347; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI2073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 2 A; 1 C; 6 G; 3 T; 0 U; 0 Other;
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI2073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 2 A; 1 C; 6 G; 3 T; 0 U; 0 Other;
 XX
 Query Match 27.9%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 3.4e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 5 CCTACGCTGA 15
 DB 11 CCTACACGTA 1
 RESULT 596
 ABI18399/c
 ID ABI18399 standard; DNA; 12 BP.
 XX
 AC ABI18399;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 318372 for detecting SNP TSC0028620.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 318372; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI2073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;
 XX
 Query Match 27.9%; Score 7.8; DB 1; Length 12;
 Best Local Similarity 81.8%; Pred. No. 3.4e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 12 TGTACAGGAG 22
 DB 12 TGTACAGGTAG 2
 RESULT 597
 ABF18031/c
 ID ABF18031 standard; DNA; 13 BP.
 XX
 AC ABF18031;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 118028 for detecting SNP TSC0029509.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX

PA (EPiG-) EPIGENOMICS AG.
 PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 118028; 29pp + Sequence Listing; German.
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 3 A; 7 C; 0 G; 3 T; 0 U; 0 Other;
 SQ Query Match 27.9%; Score 7.8; DB 1; Length 13;
 Best Local Similarity 81.8%; Pred. No. 3.8e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 12 TGTACAGGGAG 22
 DB 13 TGTAGAGGTAG 3
 RESULT 598
 ABF18030
 ID ABF18030 standard; DNA; 13 BP.
 XX AC ABF18030;
 XX 21-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 118027 for detecting SNP TSC0029509.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPiG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 118027; 29pp + Sequence Listing; German.
 CC This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 3 A; 0 C; 7 G; 3 T; 0 U; 0 Other;
 SQ Query Match 27.9%; Score 7.8; DB 1; Length 13;
 Best Local Similarity 81.8%; Pred. No. 3.8e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 12 TGTACAGGGAG 22
 DB 1 TGTAGAGGTAG 11
 RESULT 599
 ABF19283/C
 ID ABF19283 standard; DNA; 13 BP.
 XX AC ABF19283;
 XX 21-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 119280 for detecting SNP TSC0029787.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPiG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 119280; 29pp + Sequence Listing; German.
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 4 A; 3 C; 1 G; 4 T; 0 U; 1 Other;

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Query Match      27.9%; Score 7.8; DB 1; Length 13;
Best Local Similarity 69.2%; Pred. No. 3.8e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      12 TGTACAGGGAGTC 24
        ||||| |||||
Db      13 TGTAAACGTAGTY 1

RESULT 600
ABF4695/c
ID ABF44695 standard; DNA; 13 BP.
AC ABF44695;
XX
DT 21-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 144692 for detecting SNP TSC0036396.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 144692; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 4 C; 1 G; 3 T; 0 U; 1 Other;
XX
Query Match      27.9%; Score 7.8; DB 1; Length 13;
Best Local Similarity 69.2%; Pred. No. 3.8e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      12 TGTACAGGGAGTC 24
        ||||| |||||
Db      13 TGTAGACGTAGTY 1

RESULT 601
ABF19282
ID ABF19282 standard; DNA; 13 BP.

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XX ABF19282;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 119279 for detecting SNP TSC0029787.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 119279; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 1 C; 3 G; 4 T; 0 U; 1 Other;
XX
Query Match      27.9%; Score 7.8; DB 1; Length 13;
Best Local Similarity 69.2%; Pred. No. 3.8e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      12 TGTACAGGGAGTC 24
        ||||| |||||
Db      1 TGTAAACGTAGTY 13

RESULT 602
ABF4694
ID ABF44694 standard; DNA; 13 BP.
XX
AC ABF44694;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 144691 for detecting SNP TSC0036396.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX

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CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 3 A; 4 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 27.9%; Score 7.8; DB 1; Length 13;
 Best Local Similarity 81.8%; Pred. No. 3.8e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CTACGTTTACA 17
 |||||
 Db 3 CTCCTGTTTACA 13

RESULT 605
 ADB01855/c
 ID ADB01855 standard; DNA; 25 BP.
 XX
 AC ADB01855;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human MD23 scanning oligonucleotide SEQ ID 2841.
 XX
 KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.
 XX

OS Homo sapiens.
 XX
 PN EP1281758-A2.
 XX
 PD 05-FEB-2003.
 XX
 PF 30-JUL-2002; 2002EP-00016874.
 XX
 PR 02-AUG-2001; 2001US-00922181.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Shannon M, Gu Y, Nguyen C;
 XX
 WPI; 2003-423107/40.
 XX

XX New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MD23,
 PT MD24, MD27 or MD212, e.g. cancer.

XX Example 8; SEQ ID NO 2841; 103pp; English.
 PS
 CC The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder,
 CC associated with decreased or increased expression or activity of MD23,
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.

XX Sequence 25 BP; 3 A; 7 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 27.9%; Score 7.8; DB 1; Length 25;
 Best Local Similarity 63.2%; Pred. No. 5.3e+02;
 Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 GCCCTACGTTACAGGGAG 22
 |||||
 Db 23 GCACCTCGCTGCACACGTAG 5

RESULT 606
 ADB01856/c
 ID ADB01856 standard; DNA; 25 BP.
 XX
 AC ADB01856;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human MD23 scanning oligonucleotide SEQ ID 2842.
 XX
 KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.
 XX

OS Homo sapiens.
 XX
 PN EP1281758-A2.
 XX
 PD 05-FEB-2003.
 XX
 PF 30-JUL-2002; 2002EP-00016874.
 XX
 PR 02-AUG-2001; 2001US-00922181.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Shannon M, Gu Y, Nguyen C;
 XX
 WPI; 2003-423107/40.
 XX
 DR New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MD23,
 PT MD24, MD27 or MD212, e.g. cancer.

XX Example 8; SEQ ID NO 2842; 103pp; English.

XX The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder,
 CC associated with decreased or increased expression or activity of MD23,
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.

XX Sequence 25 BP; 3 A; 7 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 27.9%; Score 7.8; DB 1; Length 25;
 Best Local Similarity 63.2%; Pred. No. 5.3e+02;
 Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 GCCCTACGTTACAGGGAG 22
 |||||
 Db 22 GCACCTCGCTGCACACGTAG 4

XX OS Homo sapiens.
 XX PN EP1281758-A2.
 XX PD 05-FEB-2003.
 XX PF 30-JUL-2002; 2002EP-00016874.
 XX PR 02-AUG-2001; 2001US-00922181.
 XX PA (AEOM-) AEOMICA INC.
 XX PI Shannon M, Gu Y, Nguyen C;
 XX WPI; 2003-423107/40.
 XX PT New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MD23,
 PT MD24, MD27 or MD212, e.g. cancer.
 XX Example 8; SEQ ID NO 2843; 103pp; English.
 XX The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder
 CC associated with decreased or increased expression or activity of MD23,
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.
 XX Sequence 25 BP; 4 A; 7 C; 9 G; 5 T; 0 U; 0 Other;
 SQ Query Match 27.9%; Score 7.8; DB 1; Length 25;
 Best Local Similarity 63.2%; Pred. No. 5.3e+02;
 Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 4 GCCTACGCTGACAGGAG 22
 DB |||||
 21 GCCTCGCTGCACACGTAG 3
 RESULT 610
 ADB01858/c
 ID ADB01858 standard; DNA; 25 BP.
 AC ADB01858;
 XX 20-NOV-2003 (first entry)
 DT Human MD23 scanning oligonucleotide SEQ ID 2844.
 DE Cytostatic; immunostimulant; gene therapy; vaccine; human;
 XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.
 XX Homo sapiens.
 OS EP1281758-A2.
 PN 05-FEB-2003.
 PD 30-JUL-2002; 2002EP-00016874.
 PF

XX PR 02-AUG-2001; 2001US-00922181.
 XX PA (AEOM-) AEOMICA INC.
 XX PI Shannon M, Gu Y, Nguyen C;
 XX WPI; 2003-423107/40.
 XX PT New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MD23,
 PT MD24, MD27 or MD212, e.g. cancer.
 XX Example 8; SEQ ID NO 2844; 103pp; English.
 XX The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder
 CC associated with decreased or increased expression or activity of MD23,
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.
 XX Sequence 25 BP; 5 A; 6 C; 9 G; 5 T; 0 U; 0 Other;
 SQ Query Match 27.9%; Score 7.8; DB 1; Length 25;
 Best Local Similarity 63.2%; Pred. No. 5.3e+02;
 Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 4 GCCTACGCTGACAGGAG 22
 DB |||||
 20 GCCTCGCTGCACACGTAG 2
 RESULT 611
 AAF47954
 ID AAF47954 standard; DNA; 15 BP.
 XX AAF47954;
 AC AAF47954;
 XX 30-MAR-2001 (first entry)
 DT IGFBP3 oligonucleotide #1374.
 DE Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiac; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth factor 1 receptor; IGF-1; pituitary;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX Homo sapiens.
 OS WO200078341-A1.
 XX 28-DEC-2000.
 XX 21-JUN-2000; 2000WO-AU000693.
 PF 21-JUN-1999; 99US-0140345P.
 PR (MURD-) MURDOCH CHILDRENS RES INST.
 XX PA

XX Wright CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisenescence nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX Example 7; Page 53; 201pp; English.
 XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisenescence oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisenescence
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX Sequence 15 BP; 3 A; 8 C; 2 G; 2 T; 0 U; 0 Other;
 SQ Query Match 27.1%; Score 7.6; DB 1; Length 15;
 Best Local Similarity 71.4%; Pred. No. 4.8e+02;
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 5 CCTACGCTGACAG 18
 Db 2 CACTCCCGTACAG 15
 RESULT 612
 AAF47955
 ID AAF47955 standard; DNA; 15 BP.
 AC AAF47955;
 XX 30-MAR-2001 (first entry)
 DT IGFBP3 oligonucleotide #1375.
 DE Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX Homo sapiens.
 OS WO200078341-A1.
 PN 28-DEC-2000.
 XX 21-JUN-2000; 2000WO-AU000693.
 PF 21-JUN-1999; 99US-0140345P.
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 PA Wright CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisenescence nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX Example 7; Page 53; 201pp; English.
 XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisenescence oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisenescence
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX Sequence 15 BP; 3 A; 7 C; 2 G; 3 T; 0 U; 0 Other;
 SQ Query Match 27.1%; Score 7.6; DB 1; Length 15;
 Best Local Similarity 71.4%; Pred. No. 4.8e+02;
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 5 CCTACGCTGACAG 18
 Db 1 CACTCCCGTACAG 14
 RESULT 613
 AAF47956
 ID AAF47956 standard; DNA; 15 BP.
 AC AAF47956;
 XX 30-MAR-2001 (first entry)
 DT IGFBP3 oligonucleotide #1376.
 DE Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX Homo sapiens.
 OS WO200078341-A1.
 PN 28-DEC-2000.
 XX 21-JUN-2000; 2000WO-AU000693.
 PF 21-JUN-1999; 99US-0140345P.
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 PA Wright CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisenescence nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or

PT inflammation.
 XX
 PS Example 7; Page 53; 201pp; English.
 XX
 CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for insulin-like growth factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAP45151 and AAP45153-
 CC F45361). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, seborrheoa, xeloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 3 A; 6 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 27.1%; Score 7.6; DB 1; Length 15;
 Best Local Similarity 71.4%; Pred. No. 4.8e+02;
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 7 CTACGCTGACAGG 20
 Db |||||
 2 CTCGCCGTACAGTG 15
 RESULT 614
 ABA80105/c
 ID ABA80105 standard; DNA; 17 BP.
 XX
 AC ABA80105;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE HBA2 mutation correcting oligonucleotide SEQ ID NO: 2951.
 XX
 KW Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
 KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 KW Alzheimer's disease; cytosolic; antitickling; antiataemic; haemostatic;
 KW antilipemic; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200173002-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001WO-US009761.
 XX
 PR 27-MAR-2000; 2000US-0192176P.
 PR 27-MAR-2000; 2000US-0192179P.
 PR 01-JUN-2000; 2000US-0208538P.
 PR 30-OCT-2000; 2000US-0244989P.
 XX
 XX (UYDE) UNIV DELAWARE.
 XX
 XX Kmiec EB, Gamper HB, Rice MC;
 XX WPI; 2001-639230/73.
 XX
 DR Oligonucleotide for targeted alterations of genetic sequences and for
 XX treating cystic fibrosis, comprises at least one mismatch and chemical
 PT

PT modification.
 XX
 PS Claim 7; Page 208; 294pp; English.
 XX
 CC The present invention provides single-stranded oligonucleotides which can
 CC be used for the targeted alteration of genomic sequences, where the
 CC oligonucleotide has at least one mismatch compared with the genomic
 CC sequence to be altered. In particular, these sequences are directed at
 CC the following genes: adenosine deaminase, p53, beta-globin,
 CC retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A
 CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
 CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 CC various syndromes. The present sequence is one of the gene correcting
 CC oligonucleotides of the invention
 XX
 SQ Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
 Query Match 27.1%; Score 7.6; DB 1; Length 17;
 Best Local Similarity 71.4%; Pred. No. 5.2e+02;
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 6 CCTACGCTGACAGG 19
 Db |||||
 15 CCTCCCTGGACAAG 2
 RESULT 615
 ABA80104
 ID ABA80104 standard; DNA; 17 BP.
 XX
 AC ABA80104;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE HBA2 mutation correcting oligonucleotide SRQ ID NO: 2950.
 XX
 KW Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
 KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 KW Alzheimer's disease; cytosolic; antitickling; antiataemic; haemostatic;
 KW antilipemic; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200173002-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001WO-US009761.
 XX
 PR 27-MAR-2000; 2000US-0192176P.
 PR 27-MAR-2000; 2000US-0192179P.
 PR 01-JUN-2000; 2000US-0208538P.
 PR 30-OCT-2000; 2000US-0244989P.
 XX
 XX (UYDE) UNIV DELAWARE.
 XX
 XX Kmiec EB, Gamper HB, Rice MC;
 XX WPI; 2001-639230/73.
 XX
 DR Oligonucleotide for targeted alterations of genetic sequences and for
 XX

PT treating cystic fibrosis, comprises at least one mismatch and chemical
PT modification.
XX
PS Claim 7; Page 208; 294pp; English.
XX
CC The present invention provides single-stranded oligonucleotides which can
CC be used for the targeted alteration of genomic sequences, where the
CC oligonucleotide has at least one mismatch compared with the genomic
CC sequence to be altered. In particular, these sequences are directed at
CC the following genes: adenosine deaminase, p53, beta-globin,
CC retinoblastoma, BRCA1, BRCA2, CPT2, cyclin-dependent kinase inhibitor 2A
CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
CC (UGT1), amyloid precursor protein (APP), presenilin-1 (PSEN1) and
CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
CC haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,
CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
CC various syndromes. The present sequence is one of the gene correcting
CC oligonucleotides of the invention.
XX
SQ Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 27.1%; Score 7.6; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 5.2e+02;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 6 CCTACGCTACAGG 19
Db 3 CTTCCCTGGACAG 16
RESULT 616
ADD71263
ID ADD71263 standard; DNA; 10 BP.
XX
AC ADD71263;
XX
DT 15-JAN-2004 (first entry)
XX
DE Mouse ET gene 5' splice donor site from intron 4.
XX
KW Mouse; ethenolaminephosphate cytidyl transferase; ET; ds;
KW splice donor site; antilipemic; cardiant; anorectic;
KW phosphatidylethanolamine; Zellweger's syndrome; lipid-related disease;
KW cardiovascular disease; atherosclerosis; obesity.
XX
OS Mus musculus.
XX
PN US2003194795-A1.
XX
PD 16-OCT-2003.
XX
PF 21-MAR-2002; 2002US-00101957.
XX
PR 21-MAR-2002; 2002US-00101957.
XX
PA (BAKO/) BAKOVIC M.
PA (POLO/) POLOUMIENKO A.
XX
PI Bakovic M; Poloumienko A;
XX
DR WPI; 2003-844457/78.
XX
CC New gene encoding a protein having ethanolaminephosphate
CC cytidyltransferase activity, useful for treating Zellweger's syndrome, or
CC lipid-related diseases such as cardiovascular diseases and obesity.
XX
PS Example 1; Page 6; 22pp; English.
XX
CC The invention relates to a mouse gene encoding a protein having
CC ethanolaminephosphate cytidyltransferase (ET) activity appearing as

CC ADD71226, a degenerate variant of the ET gene, or a sequence that
CC hybridises to the complement of the ET gene under stringent conditions.
CC Also included is a promoter of a human ethanolaminephosphate
CC cytidyltransferase gene appearing as ADD71227. The gene and promoter are
CC useful for producing a transgenic animal, and for identifying,
CC preventing, and treating diseases (by gene therapy) related to
CC inappropriate phosphatidylethanolamine production, e.g. Zellweger's
CC syndrome, or lipid-related diseases such as cardiovascular diseases,
CC atherosclerosis and obesity. The present sequence is a mouse ET gene 5'
CC splice donor site.
XX
SQ Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 14 TACAGGGAG 22
Db 1 TACAGGTAG 9
RESULT 617
AAZ83886/c
ID AAZ83886 standard; DNA; 10 BP.
XX
AC AAZ83886;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #3120.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-009853P.
PR 19-JUN-1998; 98US-009897P.
PR 19-JUN-1998; 98US-0090035P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
CC Isolated polynucleotides differentially expressed between metastatic and
CC non-metastatic breast cancer cells, useful for diagnosis, prevention and
CC treatment of cancer.
XX
PS Claim 1; Page 142; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.

CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 CC
 CC Sequence 10 BP; 3 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 26.4%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.3e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 ACGTGTACA 17
 |||||
 Db 10 ACCTGTACA 2

RESULT 618

AAF37857
 ID AAF37857 standard; DNA; 10 BP.

XX AAF37857;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4596.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

XX (UJJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags; useful for studying, monitoring and
 PT affecting phases of the cell cycle.

XX Example; Page 164; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention

XX Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 26.4%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 3.3e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GTGTACAGG 19
 |||||
 Db 2 GTGTACAGG 10

RESULT 619

ABH73586

ID ABH73586 standard; DNA; 12 BP.

XX ABH73586;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 273571 for detecting SNP TSC0003234.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 273571; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, AB00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but

CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

SQ Query Match 26.4%; Score 7.4; DB 1; Length 12;

Best Local Similarity 88.9%; Pred. No. 4.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TACGGTGATC 16

DB 3 TACGGTGATC 11

RESULT 620

AAQ87648
ID AAQ87648 standard; DNA; 18 BP.

XX

XX

AC AAQ87648;

XX 19-DEC-1995 (first entry)

XX Chick antisense oligonucleotide to p75 NGFR gene.

XX Oligonucleotide; antisense; down-regulation; expression; trauma;
KW nerve growth factor receptor; neurodegenerative disease; Alzheimer's;
KW Parkinson's; Huntington's disease; multiple sclerosis;
KW vascular ischaemia; stroke; ss.

XX

OS Synthetic.

XX

XX WO9511253-A1.

XX

PD 27-APR-1995.

XX

XX 18-OCT-1994; 94WO-AU000631.

XX

PR 18-OCT-1993; 93AU-00001870.

XX

PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

XX

PI Barrett GL;

XX

XX WPI; 1995-170186/22.

XX

XX Anti-sense oligo:nucleotide(s) to nerve growth factor receptor gene - of
PT p75 NGFR, down-regulate expression and enhance neurone survival; for
PT treating cerebral palsy, Alzheimer's disease, stroke, etc.

XX

PS Example 3; Page 35; 59pp; English.

XX

XX The sequence of an antisense oligonucleotide to the chick nerve growth
CC factor receptor (NGFR) gene which was used as a control for the survival
CC of mouse dorsal root ganglial (DRG) cells treated with oligonucleotides
CC AAQ87641-2. These oligonucleotides are antisense sequences directed at
CC down-regulating the expression of the gene encoding the mouse p75 NGFR
CC gene. The oligonucleotides can be used in methods to treat
CC neurodegenerative conditions associated with disease and/or trauma such
CC as Alzheimer's, Parkinson's or Huntington's disease, multiple sclerosis,
CC vascular ischaemia associated with stroke, etc

XX

SQ Sequence 18 BP; 3 A; 4 C; 7 G; 4 T; 0 U; 0 Other;

XX

XX Query Match 26.4%; Score 7.4; DB 1; Length 18;

Best Local Similarity 64.7%; Pred. No. 5.8e+02;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

XX

XX 11 GTGTACAGGGAGTCCAG 27

XX

DB 2 GTGACTCGCTGTACAG 18

XX

XX

XX

XX

RESULT 621

ABI23376

ID ABI23376 standard; DNA; 12 BP.

XX

AC ABI23376;

XX

DT 22-FEB-2002 (first entry)

XX

DE Oligonucleotide primer SEQ ID NO 323349 for detecting SNP TSC0031342.

XX

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX

OS Homo sapiens.

XX

PN WO200177384-A2.

XX

PD 18-OCT-2001.

XX

PF 06-APR-2001; 2001WO-IB000713.

XX

PR 07-APR-2000; 2000DE-01019173.

XX

PA (EPIC-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

DR WPI; 2001-657177/75.

XX

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX

PS Claim 1; SEQ ID NO 323349; 29pp + Sequence Listing; German.

XX

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -AB09989, ABF0010-ABP9989, ABH0010-ABH9989 and ABI0010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 12 BP; 2 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

XX

XX Query Match 25.7%; Score 7.2; DB 1; Length 12;

XX Best Local Similarity 75.0%; Pred. No. 4.6e+02;

XX Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

XX

QY 8 TACGGTGATCAGG 19

XX

DB 1 TACGGTGATCAGG 12

XX

XX

XX

XX

XX

XX

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XX

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XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

OS Homo sapiens.
 XX WC200177384-A2.
 XX
 XX
 PD 18-OCT-2001.
 XX
 XX
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX
 XX (EPIG-) EPIGENOMICS AG..
 PA
 XX Olek A, Piepenbrock C, Berlin K;
 PI
 XX WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PT
 XX
 XX Claim 1; SEQ ID NO 273569; 29pp + Sequence Listing; German.
 PS
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX
 SQ Sequence 12 BP; 2 A; 2 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 25.7%; Score 7.2; DB 1; Length 12;
 Best Local Similarity 75.0%; Pred. No. 4.6e+02;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 6 CCTACGCTGACA 17
 DB 12 CGTACACGTACA 1
 RESULT 623
 AAZ41746
 ID AAZ41746 standard; DNA; 12 BP.
 XX
 AC AAZ41746;
 XX
 XX 20-MAR-2003 (revised)
 DT 21-JAN-2000 (first entry)
 XX
 XX Organic material detecting primer 107.
 DE
 XX Amplification; polymerase chain reaction; PCR; microorganism; compost;
 KW detection; pollutant; soil; food; agricultural chemical; polymer;
 KW organochlorine; primer; ss.
 XX
 XX Synthetic.
 OS
 XX DEL9914461-A1.
 PN
 XX 21-OCT-1999.
 PD
 XX
 XX 30-MAR-1999; 99DE-01014461.
 PF
 XX 31-MAR-1998; 98JP-00087651.
 PR 16-MAR-1999; 99JP-00069694.
 XX
 XX (SAOL) SANYO ELECTRIC CO LTD.
 PA

PA (NORQ) SOC TECHNO-INNOVATION AGRIC FORESTY & FI.
 XX Inoue T;
 XX WPI; 1999-592157/51.
 DR
 XX Novel polymerase chain reaction method, for differentiating between
 PT microorganisms and for detecting contaminants.
 PT
 XX Example 1; Page 19; 78pp; German.
 PS
 CC This invention describes a novel method for the amplification of DNA
 CC comprising (i) preparing many primers (P) with different probabilities of
 CC amplification and (ii) simultaneous polymerase chain reaction (PCR) of
 CC many different DNA using these primers. The method is used (1) to
 CC differentiate between different microorganisms in a mixed population and
 CC (ii) to determine presence/absence of an impurity (pollutant), or its
 CC concentration, in e.g. soil, foods, compost etc., typically metals,
 CC agricultural chemicals, polymers, organochlorine compounds etc. A
 CC particular use is monitoring composting of organic material.
 CC Amplification with many primers produces a lot of information, so
 CC reliability of the test is improved, and many samples may be tested
 CC quickly. AAZ41640-241855 represent the primers described in the method of
 CC the invention. (Updated on 20-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 12 BP; 5 A; 2 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 25.7%; Score 7.2; DB 1; Length 12;
 Best Local Similarity 75.0%; Pred. No. 4.6e+02;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 11 GTGTACAGGGAG 22
 DB 1 GAGTACAGGAG 12
 RESULT 624
 AAZ41530
 ID AAZ41530 standard; DNA; 12 BP.
 XX
 AC AAZ41530;
 XX
 XX 19-JAN-2000 (first entry)
 DT
 XX Microbe detection in organic waste arbitrarily primed PCR primer #107.
 DE
 XX Microbe; detection; organic waste; arbitrarily primer PCR;
 KW random amplified polymorphic DNA; amplification; PCR primer; ss.
 XX
 XX Synthetic.
 OS
 XX JF11276176-A.
 PN
 XX 12-OCT-1999.
 PD
 XX
 XX 31-MAR-1998; 98JP-00087652.
 PF
 XX 31-MAR-1998; 98JP-00087652.
 PR
 XX (SAOL) SANYO ELECTRIC CO LTD.
 PA (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
 XX
 XX WPI; 1999-626940/54.
 DR
 XX Amplification of a DNA fragment - in order to establish the state of
 PT existence of a microbe.
 PT
 XX Claim 1; Page 9; 40pp; Japanese.
 PS
 XX A method has been developed for the amplification of a DNA fragment in
 CC which amplification is carried out on the DNA fragments of a number of
 CC different DNAs. The method comprises a PCR reaction repeatedly carrying
 CC cut a heat-denaturing step, a primer annealing step and a polymerase

CC extending step, to amplify the DNA fragments of a plural of different
 CC DNAs. The method can detect the existence of a microbe in organic waste.
 CC AAZ41424 to AAZ41639 represent PCR primers used in random amplified
 CC polymorphic DNA arbitrarily primed PCR, for the detection of microbes in
 CC organic waste
 XX
 XX Sequence 12 BP; 5 A; 2 C; 4 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 25.7%; Score 7.2; DB 1; Length 12;
 Best Local Similarity 75.0%; Pred. No. 4.6e+02;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 11 GTGTACAGGAG 22
 Db 1 GAGTACACGAG 12
 RESULT 625
 AAC97881
 ID AAC97881 standard; DNA; 12 BP.
 XX
 AC AAC97881;
 XX
 XX 28-FEB-2001 (first entry)
 DT
 DE Primer used to illustrate DNA amplification method SEQ ID 107.
 DE
 XX Primer; amplification; selective; ss.
 XX
 XX Synthetic.
 OS
 XX JP2000270867-A.
 PN
 XX 03-OCT-2000.
 PD
 XX 19-MAR-1999; 99JP-00076844.
 PF
 XX 19-MAR-1999; 99JP-00076844.
 PR
 XX (SAOL) SANYO ELECTRIC CO LTD.
 PA
 PA (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
 XX
 XX WPI; 2001-011047/02.
 DR
 XX
 XX Amplification of a DNA fragment and its apparatus.
 FT
 XX
 XX Example 1; Page 9; 32pp; Japanese.
 PS
 XX
 CC This invention relates to a method for amplifying a DNA fragment. The
 CC method comprises successive repetitions of heat-denaturing, annealing of
 CC a primer and an extending step using a DNA polymerase. The method makes
 CC use of a cDNA pool in which the primer is one primer or a pair of primer
 CC sets and has an amplification probability which allows it to amplify a
 CC DNA fragment from a limited number of the cDNAs among the DNA pool (where
 CC the limited number is in the range of 1 to 25). Also included in the
 CC invention are apparatus used for carrying out the method, a primer and a
 CC DNA polymerase and a kit used for amplifying a DNA fragment. The method
 CC can be used to amplify a limited number of cDNAs from a pool in which a
 CC wide variety of cDNAs are present. Oligonucleotides AAC97775 - AAC97990
 CC represent primers used in an example illustrating the method of the
 CC invention
 XX
 XX Sequence 12 BP; 5 A; 2 C; 4 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 25.7%; Score 7.2; DB 1; Length 12;
 Best Local Similarity 75.0%; Pred. No. 4.6e+02;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 11 GTGTACAGGAG 22
 Db 1 GAGTACACGAG 12

RESULT 626
 ABH73580/c
 ID ABH73580 standard; DNA; 12 BP.
 XX
 AC ABH73580;
 XX
 XX 22-FEB-2002 (first entry)
 DT
 DE Oligonucleotide primer SEQ ID NO 273565 for detecting SNP TSC0003234.
 DE
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 KW
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 PN
 XX 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA
 XX Olek A, Piepenbrock C, Berlin K;
 PI
 XX WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PT
 XX Claim 1; SEQ ID NO 273565; 29pp + Sequence Listing; German.
 PS
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF0010-ABF99989, ABH0010-ABH99989 and ABIC0010-ABIC2073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 12 BP; 2 A; 1 C; 4 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 25.7%; Score 7.2; DB 1; Length 12;
 Best Local Similarity 75.0%; Pred. No. 4.6e+02;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 6 CCTACGCTGACA 17
 Db 12 CATACACGTACA 1
 RESULT 627
 ABH30582/c
 ID ABH30582 standard; DNA; 13 BP.
 XX
 AC ABH30582;
 XX
 XX 22-FEB-2002 (first entry)
 DT
 DE Oligonucleotide SEQ ID NO 230559 for detecting SNP TSC0056234.
 DE
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 KW

XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB0000713.
XX PR 07-APR-2001; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 230559; 29pp + Sequence Listing; German.
XX SQ This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 4 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 25.7%; Score 7.2; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 5e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 10 CGGTGACGGGA 21
Db 13 CGTATACAGTA 2
RESULT 628
ABC62971
ID ABC62971 standard; DNA; 13 BP.
AC ABC62971;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 62988 for detecting SNP TSC0016657.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX OS
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB0000713.
XX PR 07-APR-2001; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 230559; 29pp + Sequence Listing; German.
XX SQ This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 4 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 25.7%; Score 7.2; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 5e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 10 CGGTGACGGGA 21
Db 13 CGTATACAGTA 2
RESULT 628
ABC62971
ID ABC62971 standard; DNA; 13 BP.
AC ABC62971;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 62988 for detecting SNP TSC0016657.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX OS
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB0000713.
XX PR 07-APR-2001; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 62987; 29pp + Sequence Listing; German.
XX SQ This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The

PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 62988; 29pp + Sequence Listing; German.
XX SQ This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 3 A; 4 C; 1 G; 5 T; 0 U; 0 Other;
Query Match 25.7%; Score 7.2; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 5e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 8 TACGTGTACAG 19
Db 2 TACCTTACAG 13
RESULT 629
ABC62970/C
ID ABC62970 standard; DNA; 13 BP.
XX AC ABC62970;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 62987 for detecting SNP TSC0016657.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX OS
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB0000713.
XX PR 07-APR-2001; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 62987; 29pp + Sequence Listing; German.
XX SQ This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 5 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 25.7%; Score 7.2; DB 1; Length 13;
 Best Local Similarity 75.0%; Pred. No. 5e+02;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 TACGTTACAGG 19
 |||||
 Db 12 TACCTTACAGC 1

RESULT 630

ABC62969

ID ABC62969 standard; DNA; 13 BP.

XX AC ABC62969;

XX DT 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 62986 for detecting SNP TSC0016657.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX PS Claim 1; SEQ ID NO 62986; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 3 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 25.7%; Score 7.2; DB 1; Length 13;

Best Local Similarity 75.0%; Pred. No. 5e+02;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 TACGTTACAGG 19
 |||||
 Db 2 TACCTTACAGC 13

RESULT 631

ABC62968/c

ID ABC62968 standard; DNA; 13 BP.

XX AC ABC62968;

XX DT 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 62985 for detecting SNP TSC0016657.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX PS Claim 1; SEQ ID NO 62985; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 4 A; 1 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 25.7%; Score 7.2; DB 1; Length 13;
 Best Local Similarity 75.0%; Pred. No. 5e+02;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 TACGTTACAGG 19
 |||||
 Db 12 TACCTTACAGC 1

RESULT 632

ABH30583

ID ABH30583 standard; DNA; 13 BP.

XX AC ABH30583;

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XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 230560 for detecting SNP TSC0056234.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX ZN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 230560; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ASC00010
XX CC -ASC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AS100010-AS182073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 4 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 25.7%; Score 7.2; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 5e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 CGTGATACAGGA 21
    ||| ||| |||
Db 1 CGTATACACGTA 12

RESULT 633
AAA52434
ID AAA52434 standard; DNA; 15 BP.
XX AC AAA52434;
XX DT 18-SEP-2000 (first entry)
XX DE Tdt-expressing Ramos cell VH insertion+deletion mutation, F264.
XX KW Lymphoid cell; antibody producing cell; Ramos cell; immunoglobulin M;
XX KW IgM; V gene diversity; directed constitutive hypermutation;
XX KW target sequence diversification; terminal deoxynucleotidyl transferase;
XX KW Tdt; clonal expansion; selection; heavy chain variable region; VH;
XX KW mutant; ds.
XX OS Homo sapiens.
XX OS Synthetic.

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XX PN WO200022111-A1.
XX PD 20-APR-2000.
XX PF 08-OCT-1999; 99WO-GB003358.
XX PR 09-OCT-1998; 98GB-00022104.
XX PR 13-JAN-1999; 99GB-00001141.
XX PR 09-JUN-1999; 99GB-00013435.
XX PA (MEDI-) MEDICAL RES COUNCIL.
XX PI Sale JE, Neuberger MS, Cumbers SJ;
XX DR WPI; 2000-317971/27.
XX PT Lymphoid cell line preparation useful for producing gene products having
XX PT desired activity, involves screening and selecting cells having ongoing
XX PT target sequence diversification and higher mutation rates.
XX PS Example 4; Fig 6; 69pp; English.
XX CC The invention relates to a method of preparing a lymphoid cell line
XX CC capable of directed constitutive hypermutation of a target
XX CC nucleic acid region. The method comprises screening a cell population for
XX CC ongoing target sequence diversification and selecting a cell in which the
XX CC rate of target nucleic acid mutation exceeds that of other nucleic acid
XX CC mutation by a factor of 100 or more. The invention also relates to a
XX CC method for preparing a gene product with a desired activity, comprising
XX CC expressing a nucleic acid encoding the target gene operably linked to a
XX CC sequence which directs hypermutation e.g., terminal deoxynucleotidyl
XX CC transferase (Tdt), in the lymphoid cell line, and identifying a cell or
XX CC cells which express a mutated gene product with the desired activity. One
XX CC or more clonal populations of the identified cells is established, and
XX CC cells with an improved activity of interest are selected. These steps may
XX CC be iteratively repeated until a gene product with a desired activity
XX CC is obtained. The cell lines prepared according to the method of the
XX CC invention are used for directed constitutive hypermutation of a nucleic
XX CC acid region in the preparation of a gene product, preferably an enzyme or
XX CC of the invention, IgM-secreting Ramos cells were selected for use as they
XX CC undergo hypermutation during clonal expansion. This was determined on the
XX CC basis of the amount of diversity in the heavy chain variable region (VH).
XX CC Sequences AAA52366-AS2434 represent fragments of Ramos cell VH region DNA
XX CC containing mutations other than single nucleotide substitutions. The
XX CC number assigned to the mutation represents the position in the wild-type
XX CC VH DNA (AAA52364) to which the first nucleotide in the mutant fragment
XX CC corresponds. Sequences AAA52388-AS2434 represent mutations that occur in
XX CC Ramos cells which express Tdt, and sequences AAA52366-AS2487 represent
XX CC mutations that occur in non-Tdt- expressing control Ramos cells
XX SQ Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 25.7%; Score 7.2; DB 1; Length 15;
Best Local Similarity 75.0%; Pred. No. 5.6e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 11 GTGTACAGGGAG 22
    ||| ||| ||| |||
Db 3 GTGCATCGGG 14

RESULT 634
AAZ62686/C
ID AAZ62686 standard; RNA; 15 BP.
XX AC AAZ62686;
XX DT 28-MAR-2000 (first entry)
XX DE Substrate for HH ribozyme HCV-5596 which cleaves HCV RNA at nt. 5596.

```

KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
 KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
 KW autoimmune disease; ss.

OS Hepatitis C virus.

XX WO9955847-A2.

PN 04-NOV-1999.

XX 26-APR-1999; 99WO-US009027.

XX 27-APR-1998; 98US-0083217P.

PR 18-SEP-1998; 98US-0100842P.

PR 25-FEB-1999; 99US-00257608.

PR 23-MAR-1999; 99US-00274553.

XX (RIBO-) RIBOZYME PHARM INC.

XX Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;

XX WPI; 2000-062023/05.

XX Novel ribozymes for the treatment of diseases and conditions related to

PT hepatitis C infection.

XX Claim 1; Page 59; 123pp; English.

XX The present sequence represents the preferred target sequence of an
 CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
 CC the Hepatitis C virus (HCV) RNA sequence at the base position given in
 CC the descriptor line. The HCV sequence was screened for optimal ribozyme
 CC target sites using a computer folding algorithm and regions of the mRNA
 CC which did not form secondary folding structures and contained potential
 CC ribozyme cleavage sites were identified. Ribozymes were synthesised to
 CC target these sites and their activities optimised by either varying the
 CC length of the binding arms or by modification to prevent degradation by
 CC nucleases. The ribozymes of the invention inhibit gene expression and/or
 CC viral replication, and are used to treat diseases associated with
 CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
 CC hepatocellular carcinoma. The ribozymes may be used in combination with
 CC interferon to treat HCV infection, other infectious diseases, autoimmune
 CC diseases, and cancer

XX Sequence 15 BP; 2 A; 2 C; 8 G; 0 T; 3 U; 0 Other;

Query Match 25.7%; Score 7.2; DB 1; Length 15;
 Best Local Similarity 75.0%; Pred. No. 5.6e+02;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 15 ACAGGGAGTCCA 26

DB 13 ACCTGGACTCCA 2

RESULT 635

ABX00537/c

ID ABX00537 standard; RNA; 15 BP.

XX ABX00537;

XX 23-DEC-2002 (first entry)

XX Hepatitis C virus substrate #319 for HCV hammerhead ribozyme #319.

XX Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
 XX HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
 KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
 KW type I interferon; interferon alpha; interferon beta; cytostatic;
 KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
 KW substrate; hammerhead ribozyme; HH ribozyme; ss.

OS Hepatitis C virus.

XX US2002082225-A1.

PN 27-JUN-2002.

PD 23-MAR-1999; 99US-00274553.

PF 23-MAR-1999; 99US-00274553.

PR 23-MAR-1999; 99US-00274553.

XX (BLATT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

PA (ROBE/) ROBERTS B.

PA (PAVC/) PAVCO P A.

PA (MACE/) MACEJACK D.

XX Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;

XX WPI; 2002-617759/66.

XX New ribozymes targeting RNA derived from hepatitis C virus inhibit viral

PT replication and are useful to treat hepatitis C virus infections and

PT cirrhosis, liver failure or hepatocellular carcinoma.

XX Claim 1; Page 30; 80pp; English.

XX The present invention relates to enzymatic nucleic acids which
 CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
 CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
 CC (HP) motif where the binding arms comprise sequences complementary to one
 CC of the substrate sequences defined in the specification. The HCV
 CC ribozymes are useful for modulating the expression and/or replication of
 CC HCV. They can be used to treat cirrhosis, liver failure and/or
 CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
 CC a condition associated with HCV infection in conjunction with one or more
 CC other drug therapies, particularly type I interferon, especially
 CC interferon alpha, beta or gamma or consensus interferon. The present
 CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
 CC Some of the sequence data for this patent did not form part of the
 CC printed specification. The complete sequence data for this patent was
 CC obtained in electronic format directly from the USPTO web site at
 CC seqdata.uspto.gov/psipsDIDEntry.html

XX Sequence 15 BP; 2 A; 2 C; 8 G; 0 T; 3 U; 0 Other;

Query Match 25.7%; Score 7.2; DB 1; Length 15;
 Best Local Similarity 75.0%; Pred. No. 5.6e+02;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 15 ACAGGGAGTCCA 26

DB 13 ACCTGGACTCCA 2

RESULT 636

AAF43233

ID AAF43233 standard; DNA; 10 BP.

XX AAF43233;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11372.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

OS Saccharomyces cerevisiae.

XX WO200077214-A2.

PN 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.
 XX 16-JUN-1999; 99US-00335032.
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX Velculescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 XX gene expression (SAGE) tags, useful for studying, monitoring and
 XX affecting phases of the cell cycle.
 XX Example; Page 356; 419pp; English.
 XX The present invention describes an isolated DNA molecule comprising a
 XX coding sequence of a yeast gene selected from a group of 745 NORF (not
 XX previously assigned open reading frame; or nonannotated ORF) genes
 XX comprising a SAGE (serial analysis of gene expression) tag. Also
 XX described are: (1) a method (M1) of using NORF genes to affect the cell
 XX cycle comprising administering a NORF gene whose expression varies by at
 XX least 10% between any two phases of the cell cycle selected from log
 XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
 XX antifungal drugs comprising: (a) contacting a test substance with a yeast
 XX cell; and (b) monitoring expression of a NORF gene whose expression
 XX varies as in M1, where a test substance which modifies the expression of
 XX the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 XX identifying human genes which are involved in cell cycle progression
 XX comprising contacting human DNA with a probe which comprises at least 10
 XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
 XX and (4) a method (M4) for identifying a candidate drug as a member of a
 XX class of drugs having a characteristic effect on gene expression in a
 XX yeast cell comprising contacting a yeast cell with a candidate drug and
 XX monitoring expression in the yeast cell of at least 1 NORF gene whose
 XX expression is affected by the class of drugs. The NORF genes may be used
 XX to study, monitor and affect phases of the cell cycle, the differentially
 XX expressed genes may be used as markers of phases of the cell cycle. The
 XX methods may be used to identify candidate drugs which affect the cell
 XX cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 XX represent SAGE tags used in the exemplification of the present invention.
 XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 XX method, in the exemplification of the present invention
 XX Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
 XX
 XX Query Match 25.0%; Score 7; DB 1; Length 10;
 XX Best Local Similarity 100.0%; Pred. No. 4e+02; Indels 0; Gaps 0;
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 19 GGAGTCC 25
 Db 2 GGAGTCC 8
 |||||
 |||||
 RESULT 637
 AAF36719
 ID AAF36719 standard; DNA; 10 BP.
 XX AAF36719;
 XX 23-MAR-2001 (first entry)
 XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3458.
 XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 XX not previously assigned open reading frame; nonannotated ORF; SAGE;
 XX serial analysis of gene expression; antifungal; tag; identification;
 XX linker; PCR primer; ds.
 XX Saccharomyces cerevisiae.
 XX OS
 XX

PN WO200077214-A2.
 XX 21-DEC-2000.
 XX 14-JUN-2000; 2000WO-US016223.
 XX 16-JUN-1999; 99US-00335032.
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX Velculescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 XX gene expression (SAGE) tags, useful for studying, monitoring and
 XX affecting phases of the cell cycle.
 XX Example; Page 123; 419pp; English.
 XX The present invention describes an isolated DNA molecule comprising a
 XX coding sequence of a yeast gene selected from a group of 745 NORF (not
 XX previously assigned open reading frame; or nonannotated ORF) genes
 XX comprising a SAGE (serial analysis of gene expression) tag. Also
 XX described are: (1) a method (M1) of using NORF genes to affect the cell
 XX cycle comprising administering a NORF gene whose expression varies by at
 XX least 10% between any two phases of the cell cycle selected from log
 XX phase, S phase and G2/M; (2) a method (M2) for screening candidate
 XX antifungal drugs comprising: (a) contacting a test substance with a yeast
 XX cell; and (b) monitoring expression of a NORF gene whose expression
 XX varies as in M1, where a test substance which modifies the expression of
 XX the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 XX identifying human genes which are involved in cell cycle progression
 XX comprising contacting human DNA with a probe which comprises at least 10
 XX contiguous nucleotides of a NORF gene whose expression varies as in M1;
 XX and (4) a method (M4) for identifying a candidate drug as a member of a
 XX class of drugs having a characteristic effect on gene expression in a
 XX yeast cell comprising contacting a yeast cell with a candidate drug and
 XX monitoring expression in the yeast cell of at least 1 NORF gene whose
 XX expression is affected by the class of drugs. The NORF genes may be used
 XX to study, monitor and affect phases of the cell cycle, the differentially
 XX expressed genes may be used as markers of phases of the cell cycle. The
 XX methods may be used to identify candidate drugs which affect the cell
 XX cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 XX represent SAGE tags used in the exemplification of the present invention.
 XX AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 XX method, in the exemplification of the present invention
 XX Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;
 XX
 XX Query Match 25.0%; Score 7; DB 1; Length 10;
 XX Best Local Similarity 100.0%; Pred. No. 4e+02; Indels 0; Gaps 0;
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GGGCCCT 8
 Db 3 GGGCCCT 9
 |||||
 |||||
 RESULT 638
 ABQ86579/c
 ID ABQ86579 standard; cDNA; 11 BP.
 XX ABQ86579;
 XX 10-SEP-2002 (first entry)
 XX Human skin stress/ageing related EST SEQ ID NO 334.
 XX Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 XX OS
 XX

PN WO200253773-A2.
 XX 11-JUL-2002.
 XX
 XX
 XX 20-DEC-2001; 2001WO-EP015178.
 XX
 XX 03-JAN-2001; 2001DE-01000121.
 XX (HENK) HENKEL KGAA.
 XX
 XX Petersohn D, Conradt M, Hofmann K;
 XX
 XX WPI; 2002-528865/56.
 XX
 XX Identifying genes involved in skin stress and aging, useful e.g. in
 XX screening for cosmetic or therapeutic agents, based on differential gene
 XX expression.
 XX
 XX Claim 8; Page 50; 325pp; German.
 XX
 XX The invention relates to identifying (M1) genes in vitro that, in humans
 XX or animals, are important for skin ageing and/or skin stress by serial
 XX analysis of gene expression between mixtures of transcribed and
 XX optionally translated, genetically encoded factors (A) obtained from
 XX young and aged skin, to identify that genes that show strong differential
 XX expression. (A) comprises protein or mRNAs or their fragments. (M1) is
 XX useful for: identifying markers of skin ageing and/or stress; determining
 XX skin ageing and/or stress; and identifying or determining the effects of
 XX pharmaceutical or cosmetic agents for control of skin ageing. The present
 XX sequence is one of a group of human skin ageing/stress related expressed
 XX sequence tags (ABQ86246-ABQ87680) of the invention
 XX
 XX Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
 XX
 XX Query Match 25.0%; Score 7; DB 1; Length 11;
 XX Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 19 GGAGTCC 25
 XX |||||
 XX Db 9 GGAGTCC 3
 XX
 XX RESULT 639
 XX ABV64991/c
 XX ID ABV64991 standard; cDNA; 11 BP.
 XX AC
 XX AC ABV64991;
 XX
 XX 21-OCT-2002 (first entry)
 XX
 XX Human skin EST 2777.
 XX
 XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
 XX immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 XX Homo sapiens.
 XX
 XX WO200253774-A2.
 XX 11-JUL-2002.
 XX
 XX 20-DEC-2001; 2001WO-EP015179.
 XX
 XX 03-JAN-2001; 2001DE-01000127.
 XX (HENK) HENKEL KGAA.
 XX
 XX Petersohn D, Conradt M, Hofmann K;
 XX
 XX WPI; 2002-590638/63.
 XX

PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 XX Disclosure; Page 102; 1345pp; German.
 XX
 XX The invention relates to in vitro identification (M1) of genes expressed
 XX in the skin of humans or animals by subjecting a mixture of genetically
 XX encoded factors from skin, to serial analysis of gene expression (SAGE)
 XX so as to identify skin-expressed genes and quantify their expression.
 XX (M1) is useful for identifying genes involved in skin homeostasis; to
 XX determine skin homeostasis and to test agent (A) that maintains or
 XX promotes skin homeostasis or that can be used for treating skin
 XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 XX skin. The present sequence is that of a human expressed sequence tag
 XX (EST) of the invention
 XX
 XX Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
 XX
 XX Query Match 25.0%; Score 7; DB 1; Length 11;
 XX Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 19 GGAGTCC 25
 XX |||||
 XX Db 9 GGAGTCC 3
 XX
 XX RESULT 640
 XX AAZ90850
 XX ID AAZ90850 standard; DNA; 15 BP.
 XX AC
 XX AC AAZ90850;
 XX
 XX 24-MAY-2000 (first entry)
 XX
 XX Human NR8 gene probe #78.
 XX
 XX Haemopoietin receptor family; NR8; antibody; diagnosis;
 XX blood formation disorder; fusion protein; probe; ss.
 XX
 XX Homo sapiens.
 XX
 XX WO9967290-A1.
 XX
 XX 29-DEC-1999.
 XX
 XX 23-JUN-1999; 99WO-JP003351.
 XX
 XX 24-JUN-1998; 98JP-00214720.
 XX
 XX 19-OCT-1998; 98JP-00297409.
 XX
 XX (CHUS) CHUGAI RES INST MOLECULAR MEDICINE INC.
 XX
 XX Nomura H, Maeda M;
 XX
 XX WPI; 2000-116933/10.
 XX
 XX Hemopoietin receptor protein family NR8 used for diagnosis of blood
 XX formation disorders.
 XX
 XX Example 1; Page 41; 176pp; Japanese.
 XX
 XX The invention relates to the isolation of sequences encoding human
 XX haemopoietin receptor protein family NR8 genes. The NR8 family sequences
 XX were initially searched for comparison on a nucleic acid database with
 XX the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid
 XX sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZ59258-Z59300 and AAZ90816-
 XX Z90925 represent specific examples of probe sequences used in the search.
 XX Antibodies to the NR8 family proteins are used for the diagnosis of blood
 XX formation disorders. Compounds identified as binding to the proteins are

CC used for the treatment of such disorders

XX Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 25.0%; Score 7; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 GGAGTCC 25
|||||
Db 2 GGAGTCC 8

RESULT 641

AAZ90834
ID AAZ90834 standard; DNA; 15 BP.

XX

XX AAZ90834;

XX

DT 24-MAY-2000 (first entry)

XX

DE Human NR8 gene probe #62.

XX

Haemopoietin receptor family; NR8; antibody; diagnosis;
blood formation disorder; fusion protein; probe; ss.

XX

OS Homo sapiens.

XX

PN WO9967290-A1.

XX

PD 29-DEC-1999.

XX

PF 23-JUN-1999; 99WO-JP003351.

XX

PR 24-JUN-1998; 98JP-00214720.

XX

PR 19-OCT-1998; 98JP-00297409.

XX

PA (CHUS) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX

PI Nomura H, Maeda M;

XX

DR WPI; 2000-116933/10.

XX

Haemopoietin receptor protein family NR8 used for diagnosis of blood
formation disorders.

XX

PS Example 1; Page 40; 176pp; Japanese.

XX

CC The invention relates to the isolation of sequences encoding human
CC haemopoietin receptor protein family NR8 genes. The NR8 family sequences
CC were initially searched for comparison on a nucleic acid database with
CC the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid
CC sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZ59258-259300 and AAZ90816-
CC Z90925 represent specific examples of probe sequences used in the search.
CC Antibodies to the NR8 family proteins are used for the diagnosis of blood
CC formation disorders. Compounds identified as binding to the proteins are
CC used for the treatment of such disorders

XX Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 25.0%; Score 7; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 GGAGTCC 25
|||||
Db 2 GGAGTCC 8

RESULT 642

AAZ90885

ID AAZ90885 standard; DNA; 15 BP.

XX

AC AAZ90885;

XX

DT 24-MAY-2000 (first entry)

XX

DE Human NR8 gene probe #113.

XX

Haemopoietin receptor family; NR8; antibody; diagnosis;
blood formation disorder; fusion protein; probe; ss.

XX

OS Homo sapiens.

XX

PN WO9967290-A1.

XX

PD 29-DEC-1999.

XX

PF 23-JUN-1999; 99WO-JP003351.

XX

PR 24-JUN-1998; 98JP-00214720.

XX

PR 19-OCT-1998; 98JP-00297409.

XX

PA (CHUS) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX

PI Nomura H, Maeda M;

XX

DR WPI; 2000-116933/10.

XX

Haemopoietin receptor protein family NR8 used for diagnosis of blood
formation disorders.

XX

PS Example 1; Page 43; 176pp; Japanese.

XX

CC The invention relates to the isolation of sequences encoding human
CC haemopoietin receptor protein family NR8 genes. The NR8 family sequences
CC were initially searched for comparison on a nucleic acid database with
CC the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid
CC sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZ59258-259300 and AAZ90816-
CC Z90925 represent specific examples of probe sequences used in the search.
CC Antibodies to the NR8 family proteins are used for the diagnosis of blood
CC formation disorders. Compounds identified as binding to the proteins are
CC used for the treatment of such disorders

XX Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 25.0%; Score 7; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 6e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 GGAGTCC 25

|||||

Db 2 GGAGTCC 8

RESULT 643

AAZ90922

ID AAZ90922 standard; DNA; 15 BP.

XX

AC AAZ90922;

XX

DT 24-MAY-2000 (first entry)

XX

DE Human NR8 gene probe #150.

XX

Haemopoietin receptor family; NR8; antibody; diagnosis;
blood formation disorder; fusion protein; probe; ss.

XX

OS Homo sapiens.

XX

PN WO9967290-A1.

XX

PD 29-DEC-1999.

XX

PF 23-JUN-1999; 99WO-JP003351.

XX

PR 24-JUN-1998; 98JP-00214720.
 PR 19-OCT-1998; 98JP-00297409.
 PA (CHUS) CHUGAI RES INST MOLECULAR MEDICINE INC.
 PI Nomura H, Maeda M;
 XX WPI; 2000-116933/10.
 DR Hemopoietin receptor protein family NR8 used for diagnosis of blood
 XX formation disorders.
 PT Example 1; Page 45; 176pp; Japanese.
 XX
 XX The invention relates to the isolation of sequences encoding human
 CC haemopoietin receptor protein family NR8 genes. The NR8 family sequences
 CC were initially searched for comparison on a nucleic acid database with
 CC the nucleic acid probe sequence TGGAGYNNNGAGY encoding the amino acid
 CC sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZ59258-Z59300 and AAZ90816-
 CC Z90925 represent specific examples of probe sequences used in the search.
 CC Antibodies to the NR8 family proteins are used for the diagnosis of blood
 CC formation disorders. Compounds identified as binding to the proteins are
 CC used for the treatment of such disorders
 XX
 XX Sequence 15 BP; 2 A; 4 C; 6 G; 3 T; 0 U; 0 Other;
 SQ Query Match 25.0%; Score 7; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 19 GGAGTCC 25
 DB |||||
 2 GGAGTCC 8
 RESULT 644
 ABL46308/C
 ID ABL46308 standard; DNA; 17 BP.
 XX
 XX ABL46308;
 AC
 XX 26-APR-2002 (first entry)
 DT
 XX Mouse scavenger receptor class B type 1 oligonucleotide SEQ ID NO:275.
 DE
 XX Nucleic acid accessible hybridisation site; detection; hybridisation;
 KW characterisation; identification; nucleic acid structure; diagnosis;
 KW PCR primer; probe; ss.
 XX
 XX Mus sp.
 OS Synthetic.
 XX
 XX WO200198537-A2.
 FN
 XX 27-DEC-2001.
 PD
 XX 15-JUN-2001; 2001WO-US019401.
 PF
 XX 17-JUN-2000; 2000US-0212308P.
 PR
 XX 15-JUN-2001; 2001US-00212308.
 XX
 XX (THIR-) THIRD WAVE TECHNOLOGIES INC.
 PA
 XX Lymanichev V, Allawi H, Dong F, Neri BP, Vener IT;
 PI
 XX WPI; 2002-049698/06.
 DR
 XX Identifying oligonucleotides hybridizing to nucleic acids containing
 PT secondary structure, useful in clinical diagnosis, comprises identifying
 PT primers that interact with the target to form an extension product under
 PT amplification conditions.
 XX
 XX Claim 48; Fig 79A; 409pp; English.
 PS

XX The present invention describes a method for identifying oligonucleotides
 CC with desired hybridisation properties to nucleic acid targets containing
 CC secondary structure. The method comprises amplifying a target nucleic
 CC acid having at least one accessible and one inaccessible site. Primers
 CC that form an extension product are identified as the oligonucleotides
 CC which can interact with the folded target nucleic acid. Oligonucleotides
 CC from the present invention can be used in novel detection methods for
 CC clinical diagnostic purposes, including the detection and identification
 CC of pathogenic organisms (e.g., HIV). The method allows the ability to
 CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent
 CC sequences used in the exemplification of the present invention
 XX
 XX Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;
 SQ Query Match 25.0%; Score 7; DB 1; Length 17;
 Best Local Similarity 66.7%; Pred. No. 6.4e+02;
 Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 11 GTGTACAGGAGTCC 25
 DB |||||
 15 GTAGACATAGGTCCTC 1
 RESULT 645
 AAA11710/C
 ID AAA11710 standard; DNA; 19 BP.
 XX
 XX AAA11710;
 AC
 XX 14-JUL-2000 (first entry)
 DT
 XX Human prostate-specific antigen PCR primer #4.
 DE
 XX Prostate-specific antigen; PSA; detection; prostate cancer; PCR primer;
 KW ss.
 KW Homo sapiens.
 OS
 XX JF2000069969-A.
 PN
 XX 07-MAR-2000.
 PD
 XX 28-AUG-1998; 98JP-00243419.
 PF
 XX 28-AUG-1998; 98JP-00243419.
 PR
 XX (HITB) HITACHI CHEM CO LTD.
 PA (NIID-) NIPPON IDENSHI KENKYUSHO KK.
 XX
 XX WPI; 2000-264445/23.
 DR
 XX A primer DNA and detection of an mRNA encoding a prostate-specific
 PT antigen by using it.
 PT
 XX Claim 2; Page 9; 10pp; Japanese.
 PS
 XX This invention describes novel primers used in a method of detecting an
 CC mRNA encoding prostate-specific antigen (PSA) in which cDNA synthesis is
 CC carried out by using an mRNA encoding PSA contained in a sample as the
 CC first template and then carrying out PCR using one of four described
 CC primers to generate a second template. A further a PCR is carried out to
 CC generate a third template. The primer DNA is used for the specific
 CC detection of prostate cancer. The method is sensitive and specific.
 CC AAA11707-A11710 represent the PCR primers described in the method of the
 CC invention
 XX
 XX Sequence 19 BP; 4 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
 SQ Query Match 25.0%; Score 7; DB 1; Length 19;
 Best Local Similarity 66.7%; Pred. No. 6.5e+02;
 Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 8 TACGTGTACAGGAG 22
Db 19 TCCCTGTACACCAAG 5

Best Local Similarity 80.0%; Pred. No. 4.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TACGTGTAC 17
Db 1 TCCCTGTACA 10

RESULT 646
AAF38150
ID AAF38150 standard; DNA; 10 BP.
XX AC AAF38150;
XX DT 23-MAR-2001 (first entry)
XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4889.
XX DW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX KW serial analysis of gene expression; antifungal; tag; identification;
XX KW linker; PCR primer; ds.
XX OS Saccharomyces cerevisiae.
XX PN WO200077214-A2.
XX PD 21-DEC-2000.
XX PF 14-JUN-2000; 2000WO-US016223.
XX PR 16-JUN-1999; 99US-00335032.
XX PA (UWJO) UNIV JOHNS HOPKINS.
XX PI Velculescu V, Vogelstein B, Kinzler K;
XX DR WPI; 2001-061874/07.
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
XX PT gene expression (SAGE) tags, useful for studying, monitoring and
XX PT affecting phases of the cell cycle.
XX PS Example; Page 174; 419pp; English.
XX CC The present invention describes an isolated DNA molecule comprising a
XX CC coding sequence of a yeast gene selected from a group of 745 NORF (not
XX CC previously assigned open reading frame, or nonannotated ORF) genes
XX CC comprising a SAGE (serial analysis of gene expression) tag. Also
XX CC described are: (1) a method (M1) of using NORF genes to affect the cell
XX CC cycle comprising administering a NORF gene whose expression varies by at
XX CC least 10% between any two phases of the cell cycle selected from log
XX CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX CC antifungal drugs comprising: (a) contacting a test substance with a yeast
XX CC cell; and (b) monitoring expression of a NORF gene whose expression
XX CC varies as in M1, where a test substance which modifies the expression of
XX CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX CC identifying human genes which are involved in cell cycle progression
XX CC comprising contacting human DNA with a probe which comprises at least 10
XX CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX CC and (4) a method (M4) for identifying a candidate drug as a member of a
XX CC class of drugs having a characteristic effect on gene expression in a
XX CC yeast cell comprising contacting a yeast cell with a candidate drug and
XX CC monitoring expression in the yeast cell of at least 1 NORF gene whose
XX CC expression is affected by the class of drugs. The NORF genes may be used
XX CC to study, monitor and affect phases of the cell cycle, the differentially
XX CC expressed genes may be used as markers of phases of the cell cycle. The
XX CC methods may be used to identify candidate drugs which affect the cell
XX CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
XX CC represent SAGE tags used in the exemplification of the present invention.
XX CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX CC method, in the exemplification of the present invention
XX SQ Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 24.3%; Score 6.8; DB 1; Length 10;

SQ Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 24.3%; Score 6.8; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 4.5e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 17 AGGAGTCCA 26
 Db 1 ATGGACTCCA 10

RESULT 648
 ABQ86347
 ID ABQ86347 standard; cDNA; 11 BP.
 XX
 AC ABQ86347;
 XX
 DT 10-SEP-2002 (first entry)
 XX
 DE Human skin stress/ageing related EST SEQ ID NO 102.
 XX
 KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200253773-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015178.
 XX
 PR 03-JAN-2001; 2001DE-01000121.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-528865/56.
 XX
 KW Identifying genes involved in skin stress and aging, useful e.g. in
 PT screening for cosmetic or therapeutic agents, based on differential gene
 PT expression.
 XX
 PS Claim 8; Page 41; 325pp; German.
 XX
 CC The invention relates to identifying (M1) genes in vitro that, in humans
 CC or animals, are important for skin ageing and/or skin stress by serial
 CC analysis of gene expression between mixtures of transcribed and
 CC optionally translated, genetically encoded factors (A) obtained from
 CC young and aged skin, to identify that genes that show strong differential
 CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
 CC useful for: identifying markers of skin ageing and/or stress; determining
 CC skin ageing and/or stress; and identifying or determining the effects of
 CC pharmaceutical or cosmetic agents for control of skin ageing. The present
 CC sequence is one of a group of human skin ageing/stress related expressed
 CC sequence tags (ABQ86246-ABQ87680) of the invention
 XX
 SQ Sequence 11 BP; 2 A; 4 C; 1 G; 4 T; 0 U; 0 Other;
 Query Match 24.3%; Score 6.8; DB 1; Length 11;
 Best Local Similarity 80.0%; Pred. No. 5e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TACGTGTACA 17
 Db 1 TCCCTGTACA 10

RESULT 649
 ABV68461
 ID ABV68461 standard; cDNA; 11 BP.
 XX
 AC ABV68461;

SQ Sequence 11 BP; 2 A; 4 C; 1 G; 4 T; 0 U; 0 Other;
 Query Match 24.3%; Score 6.8; DB 1; Length 11;
 Best Local Similarity 80.0%; Pred. No. 5e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TACGTGTACA 17
 Db 1 TCCCTGTACA 10

RESULT 650
 ABH89284/C
 ID ABH89284 standard; DNA; 12 BP.
 XX
 AC ABH89284;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 289277 for detecting SNP TSC0013867.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 FN WO200177384-A2.
 XX
 PN
 XX

XX 21-OCT-2002 (first entry)
 DT
 XX Human skin EST 6247.
 DE
 XX Human; skin; dermatological; vulnary; antipsoriatic; antiseborrheic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/53.
 XX
 KW In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 PS Disclosure; Page 198; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE),
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 2 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

CC represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 12 BP; 6 A; 3 C; 1 G; 2 T; 0 U; 0 Other;
Query Match 24.3%; Score 6.8; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 5.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TACGTGTACA 17
|||||
DB 3 TACGTGTACA 12

RESULT 653
AB110703
ID AB110703 standard; DNA; 12 BP.
XX AC AB110703;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 310676 for detecting SNP TSC0024049.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB0000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX
XX Claim 1; SEQ ID NO 310676; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
XX Sequence 12 BP; 4 A; 4 C; 1 G; 3 T; 0 U; 0 Other;
Query Match 24.3%; Score 6.8; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 5.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCTACCGTGA 15
|||||

DB 2 CCTACCGTGA 11
RESULT 654
AAV11115/c
ID AAV11115 standard; RNA; 13 BP.
XX
XX AAV11115;
XX
XX 25-MAR-2003 (revised)
DT 14-JUL-1998 (first entry)
XX
XX Human ribozyme target sequence from HLA-DRB 19DRB #5.
DE
XX
XX Ribozyme; target; human lymphocyte antigen; HLA-DRB; MHC allele;
KW major histocompatibility complex; cleavage; suppression; transplant;
KW incompatibility; autoimmune disease; juvenile diabetes;
KW rheumatoid arthritis; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9704087-A1.
PN
XX
XX 06-FEB-1997.
PD
XX
XX 18-JUL-1996; 96WO-EP003173.
PF
XX
XX 18-JUL-1995; 95EP-00111256.
PR
XX
XX (KRUPP/) KRUPP G.
PA (MARG/) MARG M.
PA (WEST/) WESTPHAL E.
PA (MUEL/) MUELLER-RUCHHOLTZ W.
XX
XX Krupp G, Marget M, Westphal E, Mueller-Ruchholtz W;
PI
XX
XX WPI; 1997-132628/12.
DR
XX
XX Ribozyme that cleaves specific MHC allele(s) - used to inhibit graft
PT versus host reactions, to overcome blood incompatibility and to treat
PT auto-immune disease.
XX
XX Claim 5; Fig 1; 76pp; German.

CC AAV10915-V11123 are target sequences for a novel ribozyme which cleaves
CC specific alleles from the major histocompatibility complex (MHC). This
CC ribozyme contains a catalytic region and a hybridisation region which is
CC complementary to all mRNA transcribed from vertebrate genes of a specific
CC family of closely related MHC alleles or to mRNA from a single MHC
CC allele, and is able to cleave such mRNA. The mRNA has a target region
CC which in case is essentially conserved in all genes of the family but
CC differs from genes of all other MHC alleles to such a degree that no
CC cleavage of mRNA transcribed from these other alleles occurs. This allows
CC the selective reduction or inhibition of expression of all genes of a
CC family or of a single gene. This ribozyme can be used for permanent or
CC transient suppression of expression of MHC alleles, in vivo or in vitro.
CC Specific applications are to prevent guest vs. host or host vs. guest
CC reactions, to prevent blood incompatibilities (partic. of the ABO, rhesus
CC and Kell systems) and to treat autoimmune diseases such as juvenile
CC diabetes and rheumatoid arthritis. The use of this ribozyme avoids the
CC need for immunosuppressants in transplant patients. It provides very
CC specific reduction of particular HLA molecules that cause incompatibility
CC between donor and recipient. (Updated on 25-MAR-2003 to correct PA
CC field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
XX
XX Sequence 13 BP; 4 A; 3 C; 5 G; 0 T; 1 U; 0 Other;
SQ

Query Match 24.3%; Score 6.8; DB 1; Length 13;
Best Local Similarity 80.0%; Pred. No. 5.9e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 CAGCGAGTCC 25
|||||

Db 12 CCGGATTCC 3

RESULT 655
ABC09239
ID ABC09239 standard; DNA; 13 BP.

AC ABC09239;
XX
XX 20-FEB-2002 (first entry)
DT
DE
DE Oligonucleotide SEQ ID NO 9230 for detecting SNP TSC0002450.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
PN
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX 07-APR-2000; 2000DE-01019173.
PR
XX
XX (EPIC-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 9230; 29pp + Sequence Listing; German.
PS
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 4 C; 1 G; 3 T; 0 U; 1 Other;
PS
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 24.3%; Score 6.8; DB 1; Length 13;
Best Local Similarity 80.0%; Pred. No. 5.9e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 TAGCGTAC 17
Db 2 TACACGTACA 11

RESULT 656
ABC09238/c
ID ABC09238 standard; DNA; 13 BP.
XX
XX ABC09238;
AC
XX
XX 20-FEB-2002 (first entry)
DT
DE
DE Oligonucleotide SEQ ID NO 9229 for detecting SNP TSC0002450.
XX
XX

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
PN
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX 07-APR-2000; 2000DE-01019173.
PR
XX
XX (EPIC-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 9229; 29pp + Sequence Listing; German.
PS
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 1 C; 4 G; 4 T; 0 U; 1 Other;
PS
XX
XX Query Match 24.3%; Score 6.8; DB 1; Length 13;
Best Local Similarity 80.0%; Pred. No. 5.9e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 TAGCGTAC 17
Db 12 TACACGTACA 3

RESULT 657
AAA26121/c
ID AAA26121 standard; DNA; 14 BP.
XX
XX AAA26121;
AC
XX
XX 19-JUL-2000 (first entry)
DT
XX
XX Oestrogen receptor hairpin ribozyme target sequence SEQ ID NO:2619.
DE
XX
XX Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9954459-A2.
PN
XX
XX 28-OCT-1999.
PD
XX
XX 19-APR-1999; 99WO-US008547.
PF
XX
XX

PR 20-APR-1998; 98US-0082404P.
 PR 23-JUN-1998; 98US-00103636.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Beillon L;
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerli P;
 PI Matulic-Adamic J;
 XX
 XX WPI; 2000-013248/01.
 XX
 XX New nucleic acids that interact, and optionally cleave, target sequences,
 PT used to treat cancer.
 XX
 XX Claim 79; Page 98; 148pp; English.
 XX
 CC The present invention describes nucleic acids (A) that interact stably
 CC with a target sequence and contain at least one phosphorodithioate
 CC link, having endonuclease activity. (A), and more generally any catalytic
 CC nucleic acid (A') that modulates expression of the oestrogen receptor
 CC gene, are used to treat cancer (particularly of breast or endometrium),
 CC in vivo or by transforming cells ex vivo and implanting treated cells, or
 CC for other conditions associated with levels of oestrogen receptor.
 CC Because of the high selectivity for targeted RNA, (A) can also be used to
 CC correlate inhibition of gene expression with alterations in phenotype.
 CC reagents (for RNA, in the same way that restriction endonucleases are
 CC used with DNA). The combination of modifications in (A) improves
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
 CC AAA24748 to AAA25992 represent their corresponding target sequences.
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
 CC antisense oligonucleotides used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 14 BP; 2 A; 6 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 24.3%; Score 6.8; DB 1; Length 14;
 Best Local Similarity 80.0%; Pred. No. 6.2e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 13 GTACAGGGAG 22
 Db 14 GTACACGGCG 5
 |||||
 |||||
 RESULT 658
 AAQ83430
 ID AAQ83430 standard; DNA; 14 BP.
 XX
 AC AAQ83430;
 XX
 DT 25-MAR-2003 (revised)
 DT 20-SEP-1995 (first entry)
 XX
 DE C-fos antisense oligonucleotide.
 XX
 KW c-jun; c-fos; jun-B; neuronal injury; cell death; neoplasm; antisense;
 KW phosphorothioate; ss.
 XX
 OS Synthetic.
 XX
 XX WO9502051-A2.
 FN
 PD 19-JAN-1995.
 XX
 PF 06-JUL-1994; 94WO-EF002218.
 XX
 PR 10-JUL-1993; 93EP-00111059.
 XX
 PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX Schlingensiepen G, Schlingensiepen R, Schlingensiepen K, Brysch W;
 PI WPI; 1995-066896/09.
 XX
 XX Use of antisense c-jun, c-fos or jun-B nucleic acids - for preventing and
 PT treating neuronal injury, degeneration, cell death and/or neoplasms.
 XX
 XX Claim 2; Page 65; 86pp; English.
 XX
 CC Antisense nucleic acid hybridising with an area of the mRNA and/or DNA
 CC comprising the genes c-jun, jun-B or c-fos, expression of which plays a
 CC causal role in neuronal injury, degeneration, cell death and/or
 CC neoplasms, can be used to prevent and treat such conditions. c-jun
 CC antisense sequences are described in AAQ83267-321 and AAQ83440-43; jun-B
 CC antisense sequences are described in AAQ83322-63 and AAQ83444-45; and c-
 CC fos antisense sequences are described in AAQ83364-439 and AAQ83446- 51.
 CC Preferably the antisense sequences are phosphorothioate oligonucleotides
 CC since these are not destroyed as fast by endogenous factors as naturally
 CC occurring molecules. (Updated on 25-MAR-2003 to correct FN field.)
 XX
 SQ Sequence 14 BP; 4 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 24.3%; Score 6.8; DB 1; Length 14;
 Best Local Similarity 80.0%; Pred. No. 6.2e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 11 GTGTACAGGG 20
 Db 4 GTATACAGAG 13
 |||||
 |||||
 RESULT 659
 ABJ39464/C
 ID ABL39464 standard; DNA; 15 BP.
 XX
 AC ABL39464;
 XX
 DT 22-APR-2002 (first entry)
 XX
 DE Human ETVB allele-specific oligonucleotide primer 24.
 XX
 KW Human; electron-transfer flavoprotein beta polypeptide; ETVB;
 KW electron acceptor; mitochondrial matrix; glutaric acidemia type II;
 KW novel polymorphic site; novel polymorphism; ETVB genotype; ss; GAI1;
 KW ETVB haplotype; transgenic animal; primer; probe; chromosome 19q13;
 KW primer-extension oligonucleotide; single nucleotide polymorphism; SNP.
 XX
 OS Homo sapiens.
 XX
 FN WO200202580-A2.
 XX
 PD 10-JAN-2002.
 XX
 PF 05-JUL-2001; 2001WO-US021306.
 PF
 PR 05-JUL-2000; 2000US-0215984P.
 PR
 XX (GENA-) GENAISANCE PHARM INC.
 PA
 XX Bentivegna SC, Bieglecki KM, Kazemi A, Koshy B;
 PI WPI; 2002-154722/20.
 XX
 XX Novel isolated human electron-transfer-flavoprotein, beta polynucleotide,
 PT useful for therapeutic purposes, for studying the expression and function
 PT of the polynucleotide, and for expressing the flavoprotein.
 XX
 XX Claim 17; Page 14; 143pp; English.
 XX
 CC The invention comprises DNA, cDNA and protein sequences of the human
 CC electron-transfer flavoprotein, beta polypeptide (ETFB) gene (located on
 CC chromosome 19q13.3-13.4). The invention specifically relates to the

identification of 27 novel polymorphic sites within the E7FB gene.
 Electron-transfer flavoprotein (ETF) is an obligatory electron acceptor for nine primary flavoprotein dehydrogenases and is located in the mitochondrial matrix. ETF is composed of an alpha (E7FA) and a beta (E7FB) subunit. Electrons accepted by ETF are transferred to the mitochondrial respiratory chain by ETF dehydrogenases (ETFDHs).
 Deficiency of ETF or ETFDH leads to glutaric acidemia type II (GAI). Therefore ETF is a pharmaceutically-important gene in the treatment of GAI. The novel ETF polymorphisms identified in the invention are useful for genotyping and haplotyping the E7FB gene of an individual. The ETF protein and nucleic acids of the invention are useful for studying the expression and function of ETF in vivo. The ETF protein and nucleic acids are also useful for testing the efficacy of therapeutic agents and compounds for glutaric acidemia type II. The nucleic acids of the invention are useful in the production of a transgenic animal expressing the E7FB gene. Nucleic acids ABL39414-ABL39440 represent claimed ETFB allele-specific probes. Nucleic acids ABL39441-ABL39494 represent claimed ETFB allele-specific PCR primers. Nucleic acids ABL39495-ABL39548 represent claimed ETFB primer-extension oligonucleotides

Sequence 15 BP; 3 A; 5 C; 5 G; 1 T; 0 U; 1 Other;

Query Match 24.3%; Score 6.8; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 6.4e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 19 GGAGTCCAGG 28
 |||||
 Db 10 GGACTCTGG 1

RESULT 660
 ABA03963
 ID ABA03963 standard; DNA; 15 BP.

XX AC ABA03963;

XX DT 19-FEB-2002 (first entry)

XX DE Human STK11 gene polymorphism detection ASO primer SEQ ID NO:30.

XX KW Human; STK11; serine/threonine kinase 11; polymorphism; SNP;
 KW single nucleotide polymorphism; Peutz-Jeghers Syndrome; genotyping;
 KW haplotype; generic variant; haplotyping; allele-specific oligonucleotide;
 KW ASO; primer; ss.

XX OS Homo sapiens.

XX FN WO200187906-A2.

XX PD 22-NOV-2001.

XX PF 17-MAY-2001; 2001WO-US016045.

XX PR 17-MAY-2000; 2000US-0204697P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Bieglecki KM, Chew A, Choi JY, Mandabalan K, Sausker EA;

XX DR WPI; 2002-055679/07.

XX PT Novel genetic variants of serine/threonine kinase 11 (Peutz-Jeghers syndrome) useful in studying expression and function of the protein, and for screening candidate drugs to treat diseases e.g. Peutz-Jeghers syndrome.

XX PS Claim 16; Page 13; 86pp; English.

XX CC The present invention describes a method for haplotyping the serine/threonine kinase 11 (Peutz-Jeghers syndrome) (STK11) gene of an individual. STK11 gene sequences can be used in gene therapy. The STK11 gene is useful for screening drug targeting comprising contacting STK11

CC with a candidate agent and assaying for binding activity. STK11 is useful for improving the efficiency and reliability of several steps in the discovery and development of drugs for treating diseases associated with STK11 activity, e.g. Peutz-Jeghers syndrome. The method is useful for haplotyping the STK11 gene in an individual, which can also be used in pharmaceutical research to validate STK11 as a candidate target for, and in design of clinical trials of candidate drugs for, treating a specific condition drugs or disease predicted to be associated with STK11 activity. Allele-specific oligonucleotides (ASOs) are useful as probes and primers for assaying a polymorphism in the target region. The present sequence represents an ASO primer used for detecting STK11 gene polymorphisms, which is used in the exemplification of the present invention

XX SQ Sequence 15 BP; 2 A; 6 C; 6 G; 0 T; 0 U; 1 Other;

Query Match 24.3%; Score 6.8; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 6.4e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 16 CACGGAGTCC 25
 |||||

Db 1 CACGGAGGCC 10

RESULT 661

AAA51767/c
 ID AAA51767 standard; DNA; 16 BP.

XX AC AAA51767;

XX DT 31-OCT-2000 (first entry)

XX DE CYP3A5 gene 5' flanking region forward sequencing primer 3A5p01.

XX KW CYP3A5; Cytochrome P450; transcription regulatory region; polymorphism;
 KW Activator protein-3 motif; AP-3; basic transcription element;
 KW drug metabolism; phenotype; sequencing primer; ss.

XX OS Homo sapiens.

XX FN WO200039332-A1.

XX PD 06-JUL-2000.

XX PF 22-DEC-1999; 99WO-GB004380.

XX PR 23-DEC-1998; 98GS-00028619.

XX PA (JANC) JANSSEN PHARM NV.

XX FI Paulussen ADC, Armstrong M;

XX DR WPI; 2000-452418/39.

XX PT Identifying subjects with a high drug metabolizing phenotype associated with cytochrome CYP3A5 expression for establishing whether a drug will be metabolized by the subject.

XX PS Disclosure; Page 39; 68pp; English.

XX CC Cytochrome P450 subfamily CYP3A5 transcription regulatory regions can be screened for the presence/absence of a polymorphic variant, preferably at positions -475 or -147 of the DNA of the 5' flanking region adjacent to the CYP3A5 coding sequence. The variants are present in an activator protein-3 (AP-3) motif and/or a basic transcription element (BTE). The polymorphisms cause increased CYP3A5 gene expression and this has been linked to drug metabolic activity. Screening for the presence of variants can be used to identify subjects with a high or low drug metabolizing phenotype associated with cytochrome CYP3A5 expression. Primers are used which in addition to hybridizing to the site of interest, are capable of introducing a restriction site which is absent in either the wild type sequence or polymorphic variants. Restriction enzyme cleavage analysis

CC can then be used to indicate the presence or absence of the variant. The
 CC methods are used to establish, before treatment with a drug, whether the
 CC drug will be effectively metabolized by the patient, to identify
 CC compounds and transcription factors that can bind to a DNA sequence
 CC encoding CYP3A5, diagnosing susceptibility to a disease which is caused
 CC by toxins or procarcinogens metabolized by CYP3A5 and for identifying
 CC mutagenic effects of a compound
 XX
 SQ Sequence 16 BP; 6 A; 3 C; 6 G; 1 T; 0 U; 0 Other;
 Query Match 24.3%; Score 6.8; DB 1; Length 16;
 Best Local Similarity 80.0%; Pred. No. 6.6e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 QY 7 CTACGTGTAC 16
 DB 11 CTCCTGTAC 2
 RESULT 662
 AAT77699
 ID AAT77699 standard; DNA; 19 BP.
 XX
 AC AAT77699;
 XX
 DT 15-SEP-1997 (first entry)
 XX
 DE Wheat microsatellite WMS261 left primer.
 XX
 KW Microsatellite marker; hypervariable genomic fragment; Triticum aestivum;
 KW wheat; Triticaceae; sequence tagged site; STS; primer; PCR; amplif;
 KW polymorphism; genetic analysis; hexaploid; tetraploid; mapping; ss.
 XX
 OS Synthetic.
 XX
 XX DE19525284-A1.
 XX
 XX 02-JAN-1997.
 XX
 XX 28-JUN-1995; 95DE-01025284.
 XX
 XX 28-JUN-1995; 95DE-01025284.
 XX
 XX (PFLA-) INST PFLANZENGENETIK & KULTURPFLANZENFOR.
 XX
 XX Roeder M, Plaschke J, Ganai M;
 XX
 XX WPI; 1997-053731/06.
 XX
 XX Primers for STS microsatellite markers for wheat and related species -
 XX useful for genetic mapping, analysis and labelling etc. of wheat.
 XX
 XX Claim 5; Page 8; 8pp; German.
 XX
 CC Microsatellite markers based on hypervariable genomic fragments, from
 CC Triticum aestivum (wheat) or the tribe Triticeae, consist of a sequence
 CC tagged site (STS), defined by 2 specific primers (of mean size 17-23
 CC bases) that flank a microsatellite sequence at both ends, which can be
 CC amplified to polymorphisms (PCR products of different sizes). The
 CC microsatellites are n-fold tandem repeats (n = 10 or more) of di-, tri-,
 CC or tetra-nucleotide sequences, combination microsatellite sequences or an
 CC imperfect sequence in which individual bases are mutated. The
 CC microsatellite markers can be used for genetic analysis of hexaploid and
 CC tetraploid forms of wheat and for genetic mapping or labelling of
 CC monogenic and polygenic properties, and for their selection; for
 CC analysing relationships and identifying varieties; and for evaluating
 CC varietal purity, hybrid identification and plant growth. The markers can
 CC differentiate between almost all European wheat lines and show a higher
 CC degree of DNA polymorphism than known probes for the wheat genome. They
 CC can be detected by PCR, so large numbers of samples can be analysed
 CC easily (e.g. several hundred per day). Microsatellite marker-related
 CC polymorphisms are stably inherited so can also serve as genetic markers.
 CC AAT77003-22 and AAT77535-716 are primer pairs that define the

CC microsatellite markers. WMS261 has a CT type repeat
 XX
 SQ Sequence 19 BP; 3 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 24.3%; Score 6.8; DB 1; Length 19;
 Best Local Similarity 80.0%; Pred. No. 6.7e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 QY 7 CTACGTGTAC 16
 DB 1 CTCCTGTAC 10
 RESULT 663
 ADB01852/C
 ID ADB01852 standard; DNA; 25 BP.
 XX
 AC ADB01852;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human MDZ3 scanning oligonucleotide SEQ ID 2838.
 XX
 KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.
 XX
 OS Homo sapiens.
 XX
 XX EP1281758-A2.
 XX
 PD 05-FEB-2003.
 XX
 XX 30-JUL-2002; 2002EP-00016874.
 XX
 XX 02-AUG-2001; 2001US-00922181.
 XX
 XX (AEOM-) AEOMICA INC.
 XX
 XX Shannon M, Gu Y, Nguyen C;
 XX
 XX WPI; 2003-423107/40.
 XX
 XX New zinc finger-containing proteins and nucleic acids, useful in
 XX manufacturing a medicament for treating or preventing a disorder
 XX associated with decreased or increased expression or activity of MDZ3,
 XX MDZ4, MDZ7 or MDZ12, e.g. cancer.
 XX
 XX Example 8; SEQ ID NO 2838; 103pp; English.
 XX
 CC The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
 CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
 CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
 CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder
 CC associated with decreased or increased expression or activity of MDZ3,
 CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.
 XX
 SQ Sequence 25 BP; 5 A; 6 C; 10 G; 4 T; 0 U; 0 Other;
 Query Match 24.3%; Score 6.8; DB 1; Length 25;
 Best Local Similarity 61.8%; Pred. No. 5.8e+02;
 Matches 11; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 5 CCTACGCTGTACAGGAG 22
 ||| ||| ||| |||
 Db 25 CACTCGCTGCACACGAG 8

RESULT 664

AAV11022/c
 ID AAV11022 standard; RNA; 13 BP.

XX AC AAV11022;
 XX AC

DT 25-MAR-2003 (revised)
 DT 14-JUL-1998 (first entry)

XX DE Human ribozyme target sequence from HLA-DPB 02DPB #3.

XX KW Ribozyme; target; human lymphocyte antigen; HLA-DPB; MHC allele;
 KW major histocompatibility complex; cleavage; suppression; transplant;
 KW incompatibility; autoimmune disease; juvenile diabetes;
 KW rheumatoid arthritis; ss.

XX OS Homo sapiens.

XX PN WO9704087-A1.

XX PD 06-FEB-1997.

XX PF 18-JUL-1996; 96WO-EP003173.

XX PR 18-JUL-1995; 95EP-00111256.

XX PA (KRUPP/) KRUPP G.

XX PA (MARG/) MARGET M.

XX PA (WEST/) WESTPHAL E.

XX PA (MUEL/) MUELLER-RUCHHOLTZ W.

XX PI Krupp G, Marget M, Westphal E, Mueller-Ruchholtz W;
 XX WPI; 1997-132628/12.

XX DR

XX PT Ribozyme that cleaves specific MHC allele(s) - used to inhibit graft
 PT versus host reactions, to overcome blood incompatibility and to treat
 PT autoimmune disease.

XX PS Claim 5; Fig 1; 76pp; German.

XX CC AAV10915-V11123 are target sequences for a novel ribozyme which cleaves
 CC specific alleles from the major histocompatibility complex (MHC). This
 CC ribozyme contains a catalytic region and a hybridisation region which is
 CC complementary to all mRNA transcribed from vertebrate genes of a specific
 CC family of closely related MHC alleles or to mRNA from a single MHC
 CC allele, and is able to cleave such mRNA. The mRNA has a target region
 CC which in case is essentially conserved in all genes of the family but
 CC differs from genes of all other MHC alleles to such a degree that no
 CC cleavage of mRNA transcribed from these other alleles occurs. This allows
 CC the selective reduction or inhibition of expression of all genes of a
 CC family or of a single gene. This ribozyme can be used for permanent or
 CC transient suppression of expression of MHC alleles, in vivo or in vitro.
 CC Specific applications are to prevent guest vs. host or host vs. guest
 CC reactions, to prevent blood incompatibilities (partic. of the ABO, rhesus
 CC and Kell systems) and to treat autoimmune diseases such as juvenile
 CC diabetes and rheumatoid arthritis. The use of this ribozyme avoids the
 CC need for immunosuppressants in transplant patients. It provides very
 CC specific reduction of particular HLA molecules that cause incompatibility
 CC between donor and recipient. (Updated on 25-MAR-2003 to correct PA
 CC field.) (Updated on 25-MAR-2003 to correct PI field.)

XX SQ Sequence 13 BP; 3 A; 3 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 23.6%; Score 6.6; DB 1; Length 13;
 Best Local Similarity 69.2%; Pred. No. 6.3e+02;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 9 ACGTGTCAGGGA 21
 ||| ||| ||| |||
 Db 13 ACTGGTACAGTA 1

RESULT 665

AAF47953
 ID AAF47953 standard; DNA; 15 BP.

XX AC AAF47953;
 XX AC

DT 30-MAR-2001 (first entry)
 DT

XX DE IGFBP3 oligonucleotide #1373.

XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX OS Homo sapiens.

XX PN WO200078341-A1.

XX PD 28-DEC-2000.

XX PF 21-JUN-2000; 2000WO-AU000693.

XX PR 21-JUN-1999; 99US-0140345P.

XX PA (MURD-) MURDOCH CHILDRENS RES INST.

XX PI Wright CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.

XX DR

XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

XX PS Example 7; Page 53; 201pp; English.

XX CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

XX SQ Sequence 15 BP; 3 A; 9 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 23.6%; Score 6.6; DB 1; Length 15;
 Best Local Similarity 69.2%; Pred. No. 6.9e+02;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 CCTACGCTGTACA 17
 ||| ||| ||| |||
 Db 3 CACTCCCGGTACA 15

RESULT 666
AAQ99935/c
ID AAQ99935 standard; DNA; 16 BP.
XX
AC AAQ99935;
XX
DT 07-MAY-1996 (first entry)
XX
DE Human MTS1 RT-PCR primer, X2B.
XX
DE Multiple tumour suppressor; El-alpha; diagnosis; cancer; leukaemia;
KW astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma;
KW Gene therapy; chronic; ss.
XX
OS Homo sapiens.
XX
PN WO9525429-A1.
XX
PD 28-SEP-1995.
XX
PF 17-MAR-1995; 95WO-US003316.
XX
PR 18-MAR-1994; 94US-00214581.
PR 18-MAR-1994; 94US-00214582.
PR 18-MAR-1994; 94US-00215088.
PR 14-APR-1994; 94US-00227369.
PR 01-JUN-1994; 94US-00251938.
XX
FA (MYRI-) MYRIAD GENETICS INC.
XX
PI Kamb A;
XX
DR WPI; 1995-344401/44.
XX
DT Wild-type multiple tumour suppressor (MTS) gene and mutant sequences -
PT useful in diagnosis, prognosis and therapy of human cancer, e.g. melanoma
PT or leukaemia.
XX
PS Example 12; Page 68; 156pp; English.
XX
CC The cDNA sequences encoding several multiple tumour suppressor (MTS)
CC polypeptides have been isolated and sequenced, using various sequencing
CC and amplification primers. The primer represented in this sequence was
CC used to distinguish between two different promoters of MTS1, one alpha-
CC specific and one beta-specific. MTS polypeptide-encoding cDNAs and
CC mutants of these are useful for the diagnosis or prognosis of human
CC cancer. Germ-line mutations of MTS cDNAs can be used for diagnosing
CC predisposition to melanoma, leukaemia, astrocytoma, glioblastoma,
CC lymphoma, glioma, Hodgkin's lymphoma, CLL and cancers of the pancreas,
CC thyroid, ovary, uterus, testis, kidney, stomach and rectum. The wild-type
CC gene is useful for gene therapy and MTS polypeptides may also be used for
CC protein replacement therapy. Also the polypeptides or cells contg. an
CC altered MTS gene are useful for screening for potential cancer
CC therapeutics
XX
SQ Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 23.6%; Score 6.6; DB 1; Length 16;
Best Local Similarity 69.2%; Pred. No. 7e+02;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 7 CTACGTGTACAGG 19
DB 13 CTTCCTGGACAG 1

RESULT 667
AAT00727/c
ID AAT00727 standard; DNA; 16 BP.
XX
AC AAT00727;
XX

DT 08-MAY-1996 (first entry)
XX
DE Multiple tumour suppressor 1 gene PCR primer.
XX
KW Multiple tumour suppressor; MTS1; cancer; diagnosis; assay;
KW predisposition; melanoma; leukaemia; lymphoma; prognosis; pancreas;
KW breast; thyroid; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9525813-A1.
XX
PD 28-SEP-1995.
XX
PF 17-MAR-1995; 95WO-US003537.
XX
PR 18-MAR-1994; 94US-00214582.
PR 18-MAR-1994; 94US-00215086.
PR 18-MAR-1994; 94US-00215087.
PR 14-APR-1994; 94US-00227369.
PR 01-JUN-1994; 94US-00251938.
XX
FA (UTAH) UNIV UTAH RES FOUND.
FA (MYRI-) MYRIAD GENETICS INC.
XX
PI Skolnick MH, Cannon-Albright LA, Kamb A;
XX
DR WPI; 1995-344626/44.
XX
DT Detecting polymorphism associated with cancer predisposition - also DNA,
PT vectors and host cells e.g. for gene or protein replacement therapy and
PT drug screening.
XX
PS Example 12; Page 68; 148pp; English.
XX
CC An individual can be diagnosed as having a predisposition to cancer by
CC detecting an alteration in the wild type multiple tumour suppressor (MTS)
CC gene, using gene probes which hybridise to the MTS1 gene exon 1 or exon
CC 1beta (amplified using the PCR primers AAT00724-27). The above assay can
CC also be used in the diagnosis and prognosis of melanoma, lymphoma,
CC leukaemia and pancreas, breast and thyroid cancers, etc
XX
SQ Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 23.6%; Score 6.6; DB 1; Length 16;
Best Local Similarity 69.2%; Pred. No. 7e+02;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 7 CTACGTGTACAGG 19
DB 13 CTTCCTGGACAG 1

RESULT 668
AAT69788/c
ID AAT69788 standard; DNA; 16 BP.
XX
AC AAT69788;
XX
DT 25-MAR-2003 (revised)
DT 10-SEP-1997 (first entry)
XX
DE P16 promoter primer X2B.
XX
KW Primer; polymerase chain reaction; PCR; amplification; P16; promoter; ss.
OS Synthetic.
XX
PN US5624819-A.
XX
PD 29-APR-1997.
XX
PF 07-JUN-1995; 95US-00474177.

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XX 18-MAR-1994; 94US-00214582.
PR 18-MAR-1994; 94US-00215086.
PR 18-MAR-1994; 94US-00215087.
PR 14-APR-1994; 94US-00227369.
PR 01-JUN-1994; 94US-00251938.
PR 17-MAR-1995; 95WO-US0003537.
XX (MYRI-) MYRIAD GENETICS INC.
PA (UTAH) UNIV UTAH RES FOUND.
XX Cannon-Albright LA, Kamb A, Skolnick MH;
XX WPI; 1997-258217/23.
XX Human mutant multiple tumour suppressor gene sequences - for production
PT of recombinant mutant polypeptide(s).
XX Example 12; Col 81-82; 72pp; English.
XX The present sequence is primer for the PCR amplification of the P16
CC promoter. (Updated on 25-MAR-2003 to correct PF field.)
XX Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
SQ
Query Match 23.6%; Score 6.6; DB 1; Length 16;
Best Local Similarity 69.2%; Pred. No. 7e+02;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX 7 CTACGTGTACAGG 19
Db 13 CTTCCTGGACAG 1
RESULT 669
AAV53838/c
ID AAV53838 standard; DNA; 16 BP.
XX AAV53838;
XX 04-DEC-1998 (first entry)
XX Nucleotide sequence of PCR primer 9.
XX Multiple tumour suppressor; MTS; human; cancer; hybridisation;
XX somatic mutation; gene therapy; PCR; primer; amplification; ss.
XX Synthetic.
XX US5801236-A.
XX 01-SEP-1998.
XX 07-JUN-1995; 95US-00480810.
XX 18-MAR-1994; 94US-00214582.
PR 18-MAR-1994; 94US-00215086.
PR 18-MAR-1994; 94US-00215087.
PR 14-APR-1994; 94US-00227369.
PR 01-JUN-1994; 94US-00251938.
PR 17-MAR-1995; 95WO-US0003537.
XX (MYRI-) MYRIAD GENETICS INC.
PA Kamb A;
XX WPI; 1998-494842/42.
XX Nucleic acids based on multiple tumour suppressor, MTS, sequences -
PT useful as hybridisation probes, primers and recombinant production of MTS
PT in the diagnosis and treatment of cancers related to MTS mutation(s).
XX Example 12; Col 51; 73pp; English.

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```

XX This is the nucleotide sequence of a PCR primer used for amplification in
CC the method of the invention involving the use of the multiple tumour
CC suppressor (MTS) gene, to diagnose and treat cancer. The MTS gene is
CC useful in the diagnosis and prognosis of human cancer, e.g. by standard
CC nucleic hybridisation techniques of patient samples. The mutated
CC sequences are those that are present in somatic mutations of the gene in
CC cancers. The vectors can be used for gene therapy strategies to replace
CC function of mutated protein in patients. These can also be used to
CC construct protein mimetics, also for therapeutic strategies. In addition
CC the expression constructs can also be used for recombinant production of
CC MTS. Recombinant MTS can be used to screen for drugs to be used for
CC cancer therapy, and the protein itself may also be used to restore MTS
CC function in a cell
XX
SQ Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 23.6%; Score 6.6; DB 1; Length 16;
Best Local Similarity 69.2%; Pred. No. 7e+02;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX 7 CTACGTGTACAGG 19
Db 13 CTTCCTGGACAG 1
RESULT 670
AAV11257/c
ID AAV11257 standard; DNA; 16 BP.
XX AAV11257;
XX 15-JUL-1998 (first entry)
XX Human MTS1 and MTS1E1-beta PCR primer X2B.
XX MTS1; MTS2; multiple tumour suppressor; diagnosis; cancer;
XX germ-line mutation; familial melanoma locus; MLM; predisposition; ss.
XX Synthetic.
XX Homo sapiens.
XX US5739027-A.
XX 14-APR-1998.
XX 07-JUN-1995; 95US-00487033.
XX 18-MAR-1994; 94US-00214582.
PR 18-MAR-1994; 94US-00215086.
PR 18-MAR-1994; 94US-00215087.
PR 14-APR-1994; 94US-00227369.
PR 01-JUN-1994; 94US-00251938.
PR 17-MAR-1995; 95WO-US0003537.
XX (MYRI-) MYRIAD GENETICS INC.
XX Kamb A;
XX WPI; 1998-250421/22.
XX DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are useful
PT for the diagnosis of cancers related to MTS1E1-beta mutation(s) and their
PT treatment.
XX Example 12; Col 81-82; 72pp; English.
XX Primers AAV11256 and AAV11257 are used in the isolation of the human
CC multiple tumour suppression proteins, MTS1 and MTS1E1-beta. The MTS gene
CC locus is also referred to as the familial melanoma (MLM) gene locus,
CC located on human chromosome 9p21. Germ line mutations in MTS genes can be
CC used in the diagnosis of predisposition to cancers, e.g. melanoma,
CC leukaemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's

```

CC Lymphoma, CLL, and cancers of the pancreas, breast, thyroid, ovary,
 CC uterus, testis, kidney, stomach and rectum
 XX Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
 SQ

Query Match 23.6%; Score 6.6; DB 1; Length 16;
 Best Local Similarity 69.2%; Pred. No. 7e+02;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGG 19
 DB 13 CTTCTGGACAG 1

RESULT 671
 AAV70602/c
 ID AAV70602 standard; DNA; 16 BP.
 XX
 AC AAV70602;
 XX
 DT 20-MAR-2003 (revised)
 DT 03-FEB-1999 (first entry)
 XX
 DE PCR primer X2B for multiple tumour suppressor 2 gene.
 XX
 XX Human; multiple tumour suppressor 2 gene; MTS2; cancer; PCR primer; ss.
 KW
 XX Synthetic.
 OS Homo sapiens.
 XX
 PN US5843756-A.
 XX
 PD 01-DEC-1998.
 XX
 PF 28-JUL-1995; 95US-00508735.
 XX
 FF 17-MAR-1995; 95WO-US003316.
 PR 07-JUN-1995; 95US-00487033.
 XX
 XX (MYRI-) MYRIAD GENETICS INC.
 PA
 PI Jiang P, Kamb A, Stone S;
 XX
 XX WPI; 1999-044585/04.
 DR
 XX Mouse multiple tumour suppressor gene segment - useful for primer design.
 PT
 XX Example 14; Col 54; 80pp; English.
 PS
 XX PCR primers AAV70600-02 were used to amplify a human multiple tumour
 CC suppressor 2 (MTS2) gene. The MTS2 gene nucleotide sequence can be used
 CC to design primers to detect abnormalities i.e. polymorphisms which may
 CC predispose towards malignancies such as melanoma, leukaemia, astrocytoma,
 CC lymphoma, glioma, as well as tumours of e.g. the breast, thyroid,
 CC pancreas, uterus and kidneys. (Updated on 20-MAR-2003 to correct PF
 CC field.) (Updated on 20-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 23.6%; Score 6.6; DB 1; Length 16;
 Best Local Similarity 69.2%; Pred. No. 7e+02;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGG 19
 DB 13 CTTCTGGACAG 1

RESULT 672
 AAA95654/c
 ID AAA95654 standard; DNA; 16 BP.
 XX
 AC AAA95654;

XX 14-FEB-2001 (first entry)
 DT
 XX Human P16 promoter beta-specific primer X2B.
 DE
 XX Cytostatic; human; multiple tumour suppressor 2; MTS2; diagnostic;
 KW cancer; gene therapy; protein replacement therapy; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6090578-A.
 XX
 PD 18-JUL-2000.
 XX
 PF 08-DEC-1997; 97US-00986515.
 XX
 PR 18-MAR-1994; 94US-00214552.
 PR 18-MAR-1994; 94US-00215086.
 PR 18-MAR-1994; 94US-00215087.
 PR 14-APR-1994; 94US-00227369.
 PR 01-JUN-1994; 94US-00251338.
 PR 17-MAR-1995; 95WO-US003316.
 PR 07-JUN-1995; 95US-00480810.
 XX
 PA (MYRI-) MYRIAD GENETICS INC.
 XX
 PI Kamb A;
 XX
 XX WPI; 2000-514036/46.
 DR
 XX Novel protein composition useful in protein replacement therapy for
 PT diagnosing and treating cancer comprises a specific weight percent of
 PT human multiple tumor suppressor 1 polypeptide.
 XX
 PS Example 12; Col 49; 72pp; English.
 XX
 CC The invention relates to the isolation of the gene encoding the human
 CC multiple tumour suppressor 1 (MTS1) (AA95633). The MTS1 protein has a
 CC cytotstatic activity and is used in protein replacement therapy. This
 CC sequence is a PCR primer used in the amplification of the beta-specific
 CC form of the p16 promoter. MTS1 is useful in diagnosing human cancers such
 CC as (ocular) melanoma, leukemia, astrocytoma, glioblastoma, lymphoma,
 CC glioma, Hodgkin's lymphoma, multiple myeloma, sarcoma, myosarcoma,
 CC cholangiocarcinoma, squamous cell carcinoma, CLL, and cancers of
 CC pancreas, breast, stomach, brain, prostate, bladder, thyroid, ovary,
 CC uterus, testis, kidney, colon and rectum. The MTS1 gene and protein is
 CC useful in gene therapy, protein replacement therapy and protein mimetic
 CC studies
 XX
 SQ Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 23.6%; Score 6.6; DB 1; Length 16;
 Best Local Similarity 69.2%; Pred. No. 7e+02;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGG 19
 DB 13 CTTCTGGACAG 1

RESULT 673
 AAZ48793/c
 ID AAZ48793 standard; cDNA; 16 BP.
 XX
 AC AAZ48793;
 XX
 DT 21-MAR-2000 (first entry)
 XX
 DE PCR primer for human MTS1E1beta coding sequence.
 XX
 KW MTS; human; polymorphism detection; cancer predisposition; astrocytoma;
 KW Multiple tumour suppressor gene; melanoma; leukaemia; glioblastoma;
 KW lymphoma; glioma; Hodgkin's lymphoma; chronic lymphocytic leukaemia;

therapy; MTS1Elbeta; PCR primer; ss.
 KW XX
 OS XX
 XX XX
 FN US5989815-A.
 XX XX
 PD 23-NOV-1999.
 XX XX
 PF 29-APR-1997; 97US-00848251.
 XX XX
 PR 18-MAR-1994; 94US-00214582.
 PR 18-MAR-1994; 94US-00215086.
 PR 18-MAR-1994; 94US-00215087.
 PR 14-APR-1994; 94US-00227369.
 PR 01-JUN-1994; 94US-00251938.
 PR 17-MAR-1995; 95WO-US003537.
 PR 07-JUN-1995; 95US-00474083.
 XX XX
 PA (UTAH) UNIV UTAH RES FOUND.
 PA (MYRI-) MYRIAD GENETICS INC.
 XX XX
 PI Skolnick MH, Cannon-Albright LA, Kamb A;
 XX XX
 XX WPI; 2000-070785/06.
 DR XX
 XX
 XX Diagnosing a polymorphism associated with a predisposition for cancer.
 XX XX
 PS Example 12; Col 48; 74pp; English.
 XX XX
 CC This sequence is a PCR primer for DNA encoding human MTS1Elbeta. The
 CC invention relates to a method for diagnosing a polymorphism associated
 CC with a predisposition to cancer by detecting a germ-line alteration of a
 CC wild-type Multiple Tumour Suppressor (MTS) gene or its expression
 CC products in a human sample. The method comprises detecting a germ-line
 CC alteration of a wild-type MTS gene or its expression products in a human
 CC sample, the alteration indicating a predisposition to at least one of the
 CC cancers. The cancer is selected from melanoma, leukaemia, astrocytoma,
 CC glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, chronic lymphocytic
 CC leukaemia (CLL), and cancers of the pancreas, breast, thyroid, ovary,
 CC uterus, testis, kidney, stomach and rectum. The method may be used as
 CC basis for developing very important diagnostic tests capable of
 CC predicting the predisposition to cancer. The MTS gene is involved in the
 CC progression of multiple tumour types and may provide means for a general
 CC anti-cancer therapy by virtue of its ability to suppress tumour growth
 XX XX
 SQ Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 23.6%; Score 6.6; DB 1; Length 16;
 Best Local Similarity 69.2%; Pred. No. 7e+02;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 7 CTACGTGTACAGG 19
 DB 13 CTTCCTGGACAGC 1
 RESULT 674
 AAZ39993/c
 ID AAZ39993 standard; DNA; 16 BP.
 XX XX
 AC AAZ39993;
 XX XX
 DT 11-FEB-2000 (first entry)
 XX XX
 PF PCR primer for human multiple tumour suppressor 1 coding sequence.
 XX XX
 DE Multiple tumour suppressor; MTS; human; diagnosis; Hodgkin's lymphoma;
 KW cancer predisposition; melanoma; leukaemia; lymphoma; glioma; MTS1;
 KW PCR primer; ss.
 XX XX
 OS Synthetic.
 OS Homo sapiens.
 XX XX

FN US5994095-A.
 XX XX
 PD 30-NOV-1999.
 XX XX
 PF 07-JUN-1995; 95US-00486047.
 XX XX
 PR 18-MAR-1994; 94US-00214582.
 PR 18-MAR-1994; 94US-00215086.
 PR 18-MAR-1994; 94US-00215087.
 PR 14-APR-1994; 94US-00227369.
 PR 01-JUN-1994; 94US-00251938.
 PR 17-MAR-1995; 95WO-US003316.
 XX XX
 PA (MYRI-) MYRIAD GENETICS INC.
 XX XX
 PI Kamb A;
 XX XX
 DR WPI; 2000-038259/03.
 XX XX
 PT Multiple tumor suppressor cDNA, useful for diagnosing or determining a
 PT predisposition to cancer.
 XX XX
 PS Example 12; Col 48; 72pp; English.
 XX XX
 CC This sequence represents a PCR primer for the human multiple tumour
 CC suppressor 1 (MTS1) coding sequence. The invention relates to the human
 CC MTS2 DNA and protein sequences. The DNA sequences are useful for
 CC diagnosing or determining a predisposition to cancers e.g. melanoma,
 CC leukaemia, lymphoma, glioma, Hodgkin's lymphoma and cancers of the
 CC pancreas, breast, thyroid, ovary, kidney, uterus and stomach
 XX XX
 SQ Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 23.6%; Score 6.6; DB 1; Length 16;
 Best Local Similarity 69.2%; Pred. No. 7e+02;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 7 CTACGTGTACAGG 19
 DB 13 CTTCCTGGACAGC 1
 RESULT 675
 AAA39372/c
 ID AAA39372 standard; DNA; 16 BP.
 XX XX
 AC AAA39372;
 XX XX
 DT 12-SEP-2000 (first entry)
 XX XX
 DE Human P16 PCR primer SEQ ID NO:23.
 XX XX
 KW Human; multiple tumour suppressor; MTS; somatic mutation; cancer;
 KW diagnosis; germ line mutation; gene therapy; cytostatic; melanoma;
 KW leukaemia; astrocytoma; glioblastoma; lymphoma; glioma;
 KW Hodgkin's lymphoma; PCR primer; ss.
 XX XX
 OS Homo sapiens.
 XX XX
 PN US6060301-A.
 XX XX
 PD 09-MAY-2000.
 XX XX
 PF 14-JUL-1998; 98US-00115252.
 XX XX
 PR 18-MAR-1994; 94US-00214582.
 PR 18-MAR-1994; 94US-00215086.
 PR 18-MAR-1994; 94US-00215087.
 PR 14-APR-1994; 94US-00227369.
 PR 01-JUN-1994; 94US-00251938.
 PR 17-MAR-1995; 95WO-US003316.
 PR 07-JUN-1995; 95US-00480810.
 PR 08-DEC-1997; 97US-00986147.

```

XX PA (MYRI-) MYRIAD GENETICS INC.
XX PI Kamb A;
XX DR WPI; 2000-269915/23.
XX XX
XX PT New mutants of the human multiple tumor suppressor gene, useful as
XX PT diagnostic markers of cancer, contain specific base alterations or
XX PT deletions.
XX PS Example 12; Col 48; 72pp; English.
XX XX
XX CC The invention relates to variants (AAA1196-A11206) of the human multiple
XX CC tumour suppressor 1 (MTS1) gene (AAA11165). The variants have the
XX CC following changes relative to this sequence: A at any of positions 265,
XX CC 442, 330 and 329; T at any of positions 172, 238, 341 and 148 and
XX CC deletions of nucleotides 290-294, 172-179 or 128-129. The variants are
XX CC somatic mutations of MTS1, indicative of predisposition to melanoma and
XX CC many other cancers, so detecting them is useful for diagnosis, prognosis
XX CC and monitoring of cancer (including prenatal analysis). Cells and animals
XX CC that express the variants are useful as model systems for identifying
XX CC potential anticancer agents. This sequence represents a primer used to
XX CC screen for MTS1 Elbeta initial mRNA expression levels
XX SQ Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 23.6%; Score 6.6; DB 1; Length 16;
XX Best Local Similarity 69.2%; Pred. No. 7e+02;
XX Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 7 CTACGCTGACAGG 19
DB 13 CTTCTGGACAGC 1
XX
XX RESULT 677
XX AAF58190/c
XX ID AAF58190 standard; DNA; 16 BP.
XX XX
XX AC AAF58190;
XX XX
XX DT 23-APR-2001 (first entry)
XX XX
XX DE Primer #13.
XX XX
XX KW Human; multiple tumour suppressor; MTS; cancer; gene therapy; ss.
XX OS Homo sapiens.
XX XX
XX PN US6180776-B1.
XX XX
XX PD 30-JAN-2001.
XX XX
XX PF 22-JUL-1998; 98US-00120129.
XX XX
XX PR 18-MAR-1994; 94US-00214582.
XX PR 18-MAR-1994; 94US-00215086.
XX PR 18-MAR-1994; 94US-00215087.
XX PR 01-JUN-1994; 94US-00251938.
XX PR 17-MAR-1995; 95WO-US003316.
XX PR 07-JUN-1995; 95US-00486047.
XX XX
XX PA (MYRI-) MYRIAD GENETICS INC.
XX XX
XX PI Kamb A;
XX XX
XX DR WPI; 2001-158668/16.
XX XX
XX PT Novel multiple tumor suppressor gene useful for diagnosing, prognosing
XX PT and treating cancers, such as melanoma, leukemia, glioblastoma and
XX PT Hodgkin's lymphoma.
XX PS Example 12; Col 48; 71pp; English.
XX XX
XX CC The present invention relates to human multiple tumor suppressor-2 (MTS2)

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XX PA (MYRI-) MYRIAD GENETICS INC.
XX PI Kamb A;
XX DR WPI; 2000-349976/30.
XX XX
XX PT New vector useful for gene therapy of cancer associated with mutation in
XX PT tumor suppressor gene, comprises DNA sequence of multiple tumor
XX PT suppressor gene.
XX PS Example 12; Col 48; 71pp; English.
XX XX
XX CC The present invention describes a vector (I) comprising an isolated DNA
XX CC sequence of a multiple tumour suppressor (MTS) gene having a
XX CC polynucleotide sequence of the human MTS1E1-beta. (I) is useful for
XX CC introducing wild-type MTS function to a cancerous or pre-cancerous cell
XX CC which carries diminished or mutant MTS alleles for suppressing neoplastic
XX CC growth of the recipient cells. (I) is also useful for increasing the
XX CC level of expression of MTS gene even in tumour cells in which the mutant
XX CC gene is expressed at a normal level but the gene product is not fully
XX CC functional. A host cell transformed with (I) is useful as a model system
XX CC to study cancer remission and drug treatment which promotes such
XX CC remission. The present invention relates to somatic mutations and germ
XX CC line mutations in the MTS gene and their use in the diagnosis and
XX CC prognosis of human cancer e.g. melanoma, leukaemia, astrocytoma,
XX CC glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, and cancers of the
XX CC pancreas, breast, thyroid, ovary, uterus, testis, kidney, stomach and
XX CC rectum. The present sequence represents a PCR primer used in an example
XX CC from the present invention
XX SQ Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 23.6%; Score 6.6; DB 1; Length 16;
XX Best Local Similarity 69.2%; Pred. No. 7e+02;
XX Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 7 CTACGCTGACAGG 19
DB 13 CTTCTGGACAGC 1
XX
XX RESULT 676
XX AAA1186/c
XX ID AAA1186 standard; DNA; 16 BP.
XX XX
XX AC AAA1186;
XX XX
XX DT 11-OCT-2000 (first entry)
XX XX
XX DE Human multiple tumour suppressor 1 primer X2B.
XX XX
XX KW Variant; human; multiple tumour suppressor; MTS; mutation; melanoma;
XX KW cancer; diagnosis; PCR primer; ss.
XX OS Homo sapiens.
XX XX
XX PN US6037462-A.
XX XX
XX PD 14-MAR-2000.
XX XX
XX PF 22-JUL-1998; 98US-00120130.
XX XX
XX PR 18-MAR-1994; 94US-00214582.
XX PR 18-MAR-1994; 94US-00215086.
XX PR 18-MAR-1994; 94US-00215087.
XX PR 14-APR-1994; 94US-00227369.
XX PR 01-JUN-1994; 94US-00251938.
XX PR 17-MAR-1995; 95WO-US003316.
XX PR 07-JUN-1995; 95US-00480810.
XX XX
XX PA (MYRI-) MYRIAD GENETICS INC.
XX XX

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AC AAC83090;
XX
XX 23-FEB-2001 (first entry)
XX
XX Primer X2B used in the invention.
XX
XX MTS, Multiple Tumour Suppressor; cancer; antibody; ss.
XX
XX Homo sapiens.
XX
XX US6140473-A.
XX
XX 31-OCT-2000.
XX
XX 22-JUL-1998; 98US-00120128.
XX
XX 18-MAR-1994; 94US-00214582.
XX
XX 18-MAR-1994; 94US-00215086.
XX
XX 18-MAR-1994; 94US-00215087.
XX
XX 14-APR-1994; 94US-00227369.
XX
XX 01-JUN-1994; 94US-00251938.
XX
XX 17-MAR-1995; 95WO-US003316.
XX
XX 07-JUN-1995; 95US-00486047.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX
XX Kamb A;
XX
XX WPI; 2001-014867/02.
XX
XX New multiple tumor suppressor 2-specific antibodies useful for detecting
XX differences in the absence of the peptides or mutant gene products, or
XX for screening tissues.
XX
XX Example 12; Col 48; 71pp; English.
XX
XX The present invention relates to an antibody or its fragment that
XX specifically binds to a human multiple tumour suppressor (MTS). The
XX invention is useful for detecting differences in the absence of MTS
XX peptides, to screen a tissue or to detect mutant MTS gene products. The
XX antibodies will immunoprecipitate MTS proteins from solution as well as
XX react with MTS protein on Western or immunoblots of polyacrylamide gels
XX
XX Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 23.6%; Score 6.6; DB 1; Length 16;
XX Best Local Similarity 69.2%; Pred. No. 7e+02;
XX Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 7 CTACGTTGTACAGG 19
XX ||| ||| ||| |||
XX 13 CTTCTGGACACG 1
XX
XX RESULT 681
XX AAZ79758
XX ID AAZ79758 standard; DNA; 10 BP.
XX
XX AAZ79758;
XX
XX 10-APR-2000 (first entry)
XX
XX Human breast tumour downregulated gene SAGE tag, SEQ ID NO:49.
XX
XX SAGE tag; serial analysis of gene expression; diagnosis;
XX differential gene expression; characterisation; targeted expression;
XX tumour; cancer; immunotherapy; ss.
XX
XX Homo sapiens.
XX
XX WO9966303-A2.
XX
XX 23-DEC-1999.
XX

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XX 17-JUN-1999; 99WO-US013820.
XX
XX 19-JUN-1998; 98US-0089833P.
XX
XX 19-JUN-1998; 98US-0089844P.
XX
XX 19-JUN-1998; 98US-0089853P.
XX
XX 19-JUN-1998; 98US-0089878P.
XX
XX 19-JUN-1998; 98US-0089911P.
XX
XX 19-JUN-1998; 98US-0089922P.
XX
XX 19-JUN-1998; 98US-0089933P.
XX
XX 19-JUN-1998; 98US-0089944P.
XX
XX 19-JUN-1998; 98US-008997P.
XX
XX 19-JUN-1998; 98US-0089992P.
XX
XX 19-JUN-1998; 98US-0090000P.
XX
XX 19-JUN-1998; 98US-0090035P.
XX
XX 19-JUN-1998; 98US-0090036P.
XX
XX 19-JUN-1998; 98US-0090039P.
XX
XX 19-JUN-1998; 98US-0090040P.
XX
XX 19-JUN-1998; 98US-0090041P.
XX
XX 19-JUN-1998; 98US-0090042P.
XX
XX 19-JUN-1998; 98US-0090043P.
XX
XX 19-JUN-1998; 98US-0090044P.
XX
XX 19-JUN-1998; 98US-0090045P.
XX
XX 19-JUN-1998; 98US-0090047P.
XX
XX 19-JUN-1998; 98US-0090048P.
XX
XX 19-JUN-1998; 98US-0090072P.
XX
XX 19-JUN-1998; 98US-0090076P.
XX
XX 19-JUN-1998; 98US-0090077P.
XX
XX 19-JUN-1998; 98US-0090078P.
XX
XX 19-JUN-1998; 98US-0090079P.
XX
XX 19-JUN-1998; 98US-0090080P.
XX
XX 08-DEC-1998; 98US-0111715P.
XX
XX (GENZ ) GENZYME CORP.
XX
XX (ROBE/) ROBERTS B L.
XX
XX (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106132/09.
XX
XX New polynucleotide useful in cancer immunotherapy.
XX
XX Claim 1; Page 54; 97pp; English.
XX
XX Sequences AAZ79710-279916 represent SAGE (serial analysis of gene
XX expression) tags used to identify mRNA transcripts which are
XX differentially expressed in a variety of normal or malignant cell types.
XX Some of the transcripts correspond to known genes or ESTs (expressed
XX sequence tags) which were previously unknown to be preferentially or
XX differentially expressed in that particular cell type, while other
XX transcripts correspond to novel genes. The invention also provides a
XX nucleotide comprising a promoter sequence derived from one of the
XX differentially expressed genes, which may optionally be operably linked
XX to a foreign nucleotide sequence, and gene delivery vehicles and host
XX cells comprising the polynucleotides of the invention. A nucleotide
XX comprising sequences AAZ79710-279916 may be used in diagnostic procedures
XX to characterise a cell of a specific tissue type and to determine whether
XX it is normal or malignant. They may be used to screen for agents that
XX modulate expression of differentially expressed genes compound. The
XX promoter/foreign gene construct of the invention may be used for
XX targeted expression of the foreign gene in a particular cell type. For
XX example, a promoter derived from a gene preferentially expressed in
XX dendritic cells (antigen-presenting cells, or APCs) may be operably
XX linked to a sequence encoding an immunostimulatory molecule and a
XX sequence encoding an antigen. Such a construct could be transduced into
XX APCs and would be useful for inducing an immune response by educating
XX immune effector cells in vivo, or in cancer immunotherapy
XX
XX Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 22.9%; Score 6.4; DB 1; Length 10;
XX Best Local Similarity 87.5%; Pred. No. 5.4e+02;

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CC gene. The invention is useful for diagnosing, prognosing and treating
 CC cancers. It is also useful for screening drugs for cancer therapy and
 CC gene therapy

SQ Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 23.6%; Score 6.6; DB 1; Length 16;

Best Local Similarity 69.2%; Pred. No. 7e+02;

Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 0;

OY 7 CTACGTGTACAGG 19

Db 13 CTTCCTGGACACG 1

RESULT 678

AAS02583/c

ID AAS02583 standard; DNA; 16 BP.

XX AAS02583;

AC AAS02583;

DT 29-AUG-2001 (first entry)

DE PCR primer X2B used in analysis of multiple tumour suppressor MTS1/2.

XX Human; multiple tumour suppressor; MTS1; MTS2; therapeutic; diagnostic;

KW cancer; gene therapy; melanoma; leukaemia; astrocytoma; glioblastoma;

KW lymphoma; glioma; Hodgkin's lymphoma; chronic lymphatic leukaemia;

KW PCR primer; ss.

XX Homo sapiens.

OS US6210949-B1.

PN 03-APR-2001.

XX 30-NOV-1998; 98US-00201139.

XX 17-MAR-1995; 95WO-US003316.

PR 07-JUN-1995; 95US-00487033.

PR 28-JUL-1995; 95US-00508735.

XX (MYRI-) MYRIAD GENETICS INC.

PA Stone S, Jiang P, Kamb A;

XX WPI; 2001-280859/29.

DR New mouse multiple tumor suppressor gene, useful for diagnosing or

PT prognosing human cancer or as gene therapy for treating cancer,

PT particularly melanoma, leukemia, astrocytoma, lymphoma or cancers of the

PT pancreas or breast.

XX Example 13; Col 51; 80pp; English.

PS The sequence represents PCR primer X2B used in analysis of multiple

CC tumour suppressor MTS1 and MTS2. The MTS genes, and expression products,

CC are useful for treating, diagnosing or prognosing human cancer. In

CC particular, the MTS gene is useful for diagnosing a predisposition to or

CC as a gene therapy for melanoma, leukaemia, astrocytoma, glioblastoma,

CC lymphoma, glioma, Hodgkin's lymphoma, chronic lymphatic leukaemia (CLL),

CC or cancers of the pancreas, breast, thyroid, ovary, uterus, testis,

CC kidney, stomach or rectum. The gene may be used in both cancerous and pre

CC -cancerous cells

XX Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

SQ Query Match 23.6%; Score 6.6; DB 1; Length 16;

Best Local Similarity 69.2%; Pred. No. 7e+02;

Matches 9; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

OY 7 CTACGTGTACAGG 19

Db 13 CTTCCTGGACACG 1

RESULT 680

AAC83090/c

ID AAC83090 standard; DNA; 16 BP.

XX

Db 13 CTTCCTGGACACG 1

RESULT 679

AAD04711/c

ID AAD04711 standard; DNA; 16 BP.

XX AAD04711;

AC AAD04711;

DT 04-JUL-2001 (first entry)

XX Human MTS and MTS1beta sequence amplifying primer, X2B.

DE Human; multiple tumour suppressor; MTS1beta; cytostatic;

KW germ line mutation; gene therapy; melanoma; leukaemia; astrocytoma; CLL;

KW glioblastoma; lymphoma; glioma; Hodgkin's lymphoma; cancer; rectum;

KW pancreas; breast; thyroid; ovary; uterus; testis; kidney; stomach;

KW somatic mutation; MTS; PCR primer; ss.

XX Homo sapiens.

OS US6218146-B1.

PN 17-APR-2001.

XX 22-JUL-1998; 98US-00120131.

XX 18-MAR-1994; 94US-00214582.

PR 18-MAR-1994; 94US-00215086.

PR 18-MAR-1994; 94US-00215087.

PR 14-APR-1994; 94US-00227369.

PR 01-JUN-1994; 94US-00251938.

PR 17-MAR-1995; 95WO-US003316.

PR 07-JUN-1995; 95US-00486047.

XX (MYRI-) MYRIAD GENETICS INC.

PA Kamb A;

XX WPI; 2001-289831/30.

DR Novel multiple tumor suppressor proteins useful for diagnosis and

PT prognosis of human cancer and for screening drugs for cancer treatment.

PT Example 13; Col 52; 71pp; English.

PS The invention relates to somatic and germ line mutations in the multiple

CC tumour suppressor (MTS) gene in human cancer. The invention also relates

CC to therapy of human cancer which have a mutation in the MTS gene,

CC including gene therapy, protein replacement therapy, and protein

CC mimetics. The MTS sequences are useful for diagnosing predisposition to

CC human cancer or for diagnosing and prognosing human cancers such as

CC melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma,

CC Hodgkin's lymphoma, CLL and cancers of pancreas, breast, thyroid, ovary,

CC uterus, testis, kidney, stomach and rectum. They are also used for

CC screening drugs for cancer treatment. The present sequence is primer, X2B

CC used for amplifying human MTS and MTS1beta sequence

XX Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

SQ Query Match 23.6%; Score 6.6; DB 1; Length 16;

Best Local Similarity 69.2%; Pred. No. 7e+02;

Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 7 CTACGTGTACAGG 19

Db 13 CTTCCTGGACACG 1

RESULT 680

AAC83090/c

ID AAC83090 standard; DNA; 16 BP.

XX

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CCGTGACA 17
| | | | |
Db 2 CCGTGACA 9

RESULT 682
ABV67783
ID ABV67783 standard; cDNA; 11 BP.
XX
AC ABV67783;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 5569.
XX
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX (HENK) HENKEL KGAA.
PA Petersohn D, Conradt M, Hofmann K;
XX
PI WPI; 2002-590638/63.
XX
DR In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 179; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 3 A; 1 G; 2 T; 0 U; 0 Other;

Query Match 22.9%; Score 6.4; DB 1; Length 11;
Best Local Similarity 87.5%; Pred. No. 6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CCGTGACA 17
| | | | |
Db 4 CCGTGACA 11

RESULT 683
ABV70593/c
ID ABV70593 standard; cDNA; 11 BP.
XX
AC ABV70593;
XX

DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 8379.
XX
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX (HENK) HENKEL KGAA.
PA Petersohn D, Conradt M, Hofmann K;
XX
PI WPI; 2002-590638/63.
XX
DR In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Claim 24; Page 268; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 3 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 22.9%; Score 6.4; DB 1; Length 11;
Best Local Similarity 87.5%; Pred. No. 6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 GGAGTCCA 26
| | | | |
Db 8 GGATGCCA 1

RESULT 684
ABV63172/c
ID ABV63172 standard; cDNA; 11 BP.
XX
AC ABV63172;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 959.
XX
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.

CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 SQ Sequence 11 BP; 3 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 22.9%; Score 6.4; DB 1; Length 11;
 Best Local Similarity 87.5%; Pred. No. 6e+02; 1; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CGTGTACA 17
 | | | | |
 Db 11 CCTGTACA 4

RESULT 687
 ABH73583
 ID ABH73583 standard; DNA; 12 BP.
 XX AC ABH73583;
 XX XX
 DT 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 273568 for detecting SNP TSC0003234.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 273568; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Query Match 22.9%; Score 6.4; DB 1; Length 12;
 Best Local Similarity 87.5%; Pred. No. 6.5e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TACGTGTA 15
 | | | | |
 Db 3 TACCGGTA 10

RESULT 689
 AB116213/c
 ID AB116213 standard; DNA; 12 BP.
 XX AC AB116213;
 XX XX
 DT 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 316186 for detecting SNP TSC0027326.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Query Match 22.9%; Score 6.4; DB 1; Length 12;
 Best Local Similarity 87.5%; Pred. No. 6.5e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TACGTGTA 15
 | | | | |
 Db 3 TACCGGTA 10

RESULT 688
 AB110705/c
 ID AB110705 standard; DNA; 12 BP.
 XX AC AB110705;
 XX XX
 DT 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 310678 for detecting SNP TSC0024049.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 310678; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Query Match 22.9%; Score 6.4; DB 1; Length 12;
 Best Local Similarity 87.5%; Pred. No. 6.5e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TACGTGTA 15
 | | | | |
 Db 11 TACCGGTA 4

RESULT 689
 AB116213/c
 ID AB116213 standard; DNA; 12 BP.
 XX AC AB116213;
 XX XX
 DT 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 316186 for detecting SNP TSC0027326.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Query Match 22.9%; Score 6.4; DB 1; Length 12;
 Best Local Similarity 87.5%; Pred. No. 6.5e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TACGTGTA 15
 | | | | |
 Db 11 TACCGGTA 4

RESULT 689
 AB116213/c
 ID AB116213 standard; DNA; 12 BP.
 XX AC AB116213;
 XX XX
 DT 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 316186 for detecting SNP TSC0027326.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Query Match 22.9%; Score 6.4; DB 1; Length 12;
 Best Local Similarity 87.5%; Pred. No. 6.5e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TACGTGTA 15
 | | | | |
 Db 3 TACCGGTA 10

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 PF 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 XX methylation status.
 XX Claim 1; SEQ ID NO 316186; 29pp + Sequence Listing; German.
 PS This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB12073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 12 BP; 4 A; 1 C; 5 G; 2 T; 0 U; 0 Other;
 SQ Query Match 22.9%; Score 6.4; DB 1; Length 12;
 Best Local Similarity 87.5%; Pred. No. 6.5e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 CCCTAGCT 12
 DB 8 CCCTACTT 1
 RESULT 690
 ABC49804
 ID ABC49804 standard; DNA; 13 BP.
 XX ABC49804;
 AC 21-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 49821 for detecting SNP TSC0014053.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 PF 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 XX methylation status.
 XX Claim 1; SEQ ID NO 49822; 29pp + Sequence Listing; German.
 PS This invention describes novel oligonucleotide primers or peptide nucleic

PA (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 XX methylation status.
 XX Claim 1; SEQ ID NO 49821; 29pp + Sequence Listing; German.
 PS This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB12073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 2 A; 2 C; 4 G; 4 T; 0 U; 1 Other;
 SQ Query Match 22.9%; Score 6.4; DB 1; Length 13;
 Best Local Similarity 87.5%; Pred. No. 6.8e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 TACGGTGA 15
 DB 3 TACGGCTA 10
 RESULT 691
 ABC49805/c
 ID ABC49805 standard; DNA; 13 BP.
 XX ABC49805;
 AC 21-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 49822 for detecting SNP TSC0014053.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 PF 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 XX methylation status.
 XX Claim 1; SEQ ID NO 49822; 29pp + Sequence Listing; German.
 PS This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 4 A; 4 C; 2 G; 2 T; 0 U; 1 Other;

Query Match 22.9%; Score 6.4; DB 1; Length 13;
 Best Local Similarity 87.5%; Pred. No. 6.8e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TACGCTGA 15
 |||||
 Db 11 TACGCGTA 4

RESULT 692

ABC37725
 ID ABC37725 standard; DNA; 13 BP.

XX AC ABC37725;

XX DT 20-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 37742 for detecting SNP TSC0011735.

XX SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 XX methylation status.

XX Claim 1; SEQ ID NO 37742; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 3 A; 4 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 22.9%; Score 6.4; DB 1; Length 13;
 Best Local Similarity 87.5%; Pred. No. 6.8e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TACGCTGA 15
 |||||
 Db 5 TACGCGTA 12

RESULT 693

ABC37724/c
 ID ABC37724 standard; DNA; 13 BP.

XX AC ABC37724;

XX DT 20-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 37741 for detecting SNP TSC0011735.

XX SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 XX methylation status.

XX Claim 1; SEQ ID NO 37741; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 4 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 22.9%; Score 6.4; DB 1; Length 13;
 Best Local Similarity 87.5%; Pred. No. 6.8e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TACGCTGA 15
 |||||
 Db 9 TACGCGTA 2

RESULT 694

ID ADB00353/c
 ADB00353 standard; DNA; 17 BP.

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XX AC ADB00353;
XX DT 20-NOV-2003 (first entry)
XX DE Human MD23 scanning oligonucleotide SEQ ID 1339.
XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX KW developmental disorder; ss.
XX OS Homo sapiens.
XX PN EP1281758-A2.
XX PD 05-FEB-2003.
XX PF 30-JUL-2002; 2002EP-00016874.
XX PR 02-AUG-2001; 2001US-00922181.
XX PA (AEOM-) AEOMICA INC.
XX PI Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX DR
XX PT New zinc finger-containing proteins and nucleic acids, useful in
XX PT manufacturing a medicament for treating or preventing a disorder
XX PT associated with decreased or increased expression or activity of MD23,
XX PT MD24, MD27 or MD212, e.g. cancer.
XX PS Example 8; SEQ ID NO 1339; 103pp; English.
XX CC The present invention relates to novel human zinc finger-containing
XX CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX CC or in manufacturing a medicament for treating or preventing a disorder
XX CC associated with decreased or increased expression or activity of MD23,
XX CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX CC acids and proteins are also useful for diagnosing or monitoring a disease
XX CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX CC acids can also be used as probes to detect and characterize gross
XX CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX CC useful in constructing microarrays for measuring gene expression. The
XX CC proteins are useful as therapeutic agents for gene therapy or as
XX CC vaccines. The present sequence was used to illustrate the invention.
XX SQ Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 22.9%; Score 6.4; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 7.4e+02;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 7 CTACGTTGACAGGAG 22
Db 17 CTCGCTGCACACGTAG 2

RESULT 695
ADB00354/C
ID ADB00354 standard; DNA; 17 BP.
XX AC ADB00354;
XX DT 20-NOV-2003 (first entry)
XX DE Human MD23 scanning oligonucleotide SEQ ID 1340.
XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;

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KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX OS Homo sapiens.
XX PN EP1281758-A2.
XX PD 05-FEB-2003.
XX PF 30-JUL-2002; 2002EP-00016874.
XX PR 02-AUG-2001; 2001US-00922181.
XX PA (AEOM-) AEOMICA INC.
XX PI Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX DR
XX PT New zinc finger-containing proteins and nucleic acids, useful in
XX PT manufacturing a medicament for treating or preventing a disorder
XX PT associated with decreased or increased expression or activity of MD23,
XX PT MD24, MD27 or MD212, e.g. cancer.
XX PS Example 8; SEQ ID NO 1340; 103pp; English.
XX CC The present invention relates to novel human zinc finger-containing
XX CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX CC or in manufacturing a medicament for treating or preventing a disorder
XX CC associated with decreased or increased expression or activity of MD23,
XX CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX CC acids and proteins are also useful for diagnosing or monitoring a disease
XX CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX CC acids can also be used as probes to detect and characterize gross
XX CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX CC useful in constructing microarrays for measuring gene expression. The
XX CC proteins are useful as therapeutic agents for gene therapy or as
XX CC vaccines. The present sequence was used to illustrate the invention.
XX SQ Sequence 17 BP; 3 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 22.9%; Score 6.4; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 7.4e+02;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 7 CTACGTTGACAGGAG 22
Db 16 CTCGCTGCACACGTAG 1

RESULT 696
ADB00356/C
ID ADB00356 standard; DNA; 17 BP.
XX AC ADB00356;
XX DT 20-NOV-2003 (first entry)
XX DE Human MD23 scanning oligonucleotide SEQ ID 1342.
XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX KW developmental disorder; ss.
XX OS Homo sapiens.
XX PN EP1281758-A2.

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PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MDZ3,
XX MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
XX Example 8; SEQ ID NO 1342; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
XX encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
XX MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
XX 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MDZ3,
XX MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
XX
Query Match 22.9%; Score 6.4; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 7.4e+02;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 4 GCCTACGCTGACAGG 19
Db 17 GCACCTCGCTGCACACG 2
RESULT 697
ADB00357/c
ID ADB00357 standard; DNA; 17 BP.
XX
XX ADB00357;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MDZ3 scanning oligonucleotide SEQ ID 1343.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX EP1281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MDZ3,
XX MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
XX Example 8; SEQ ID NO 1342; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
XX encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
XX MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
XX 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MDZ3,
XX MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
XX
Query Match 22.9%; Score 6.4; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 7.4e+02;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 4 GCCTACGCTGACAGG 19
Db 17 GCACCTCGCTGCACACG 2
RESULT 698
ADB01851/c
ID ADB01851 standard; DNA; 25 BP.
XX
XX ADB01851;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MDZ3 scanning oligonucleotide SEQ ID 2837.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX EP1281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MDZ3,
XX MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
XX Example 8; SEQ ID NO 1343; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
XX encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
XX MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
XX 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MDZ3,
XX MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 2 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
XX
Query Match 22.9%; Score 6.4; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 7.4e+02;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 4 GCCTACGCTGACAGG 19
Db 16 GCACCTCGCTGCACACG 1
RESULT 699
ADB01851/c
ID ADB01851 standard; DNA; 25 BP.
XX
XX ADB01851;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MDZ3 scanning oligonucleotide SEQ ID 2837.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX EP1281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MDZ3,
XX MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
XX Example 8; SEQ ID NO 1343; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
XX encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
XX MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
XX 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MDZ3,
XX MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 2 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
XX
Query Match 22.9%; Score 6.4; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 7.4e+02;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 4 GCCTACGCTGACAGG 19
Db 16 GCACCTCGCTGCACACG 1

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XX PS Example 8; SEQ ID NO 2837; 103pp; English.
XX CC The present invention relates to novel human zinc finger-containing
XX CC proteins and their coding sequences; MD23, MD24, MD27, MD212. MD23 is
XX CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX CC or in manufacturing a medicament for treating or preventing a disorder,
XX CC associated with decreased or increased expression or activity of MD23,
XX CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX CC acids and proteins are also useful for diagnosing or monitoring a disease
XX CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX CC acids can also be used as probes to detect and characterize gross
XX CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX CC useful in constructing microarrays for measuring gene expression. The
XX CC proteins are useful as therapeutic agents for gene therapy or as
XX CC vaccines. The present sequence was used to illustrate the invention.
XX SQ Sequence 25 BP; 6 A; 6 C; 9 G; 4 T; 0 U; 0 Other;

Query Match      22.9%; Score 6.4; DB 1; Length 25;
Best Local Similarity 62.5%; Pred. No. 5.9e+02;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 7 CTACGCTGACAGGAG 22
Db 24 CTCGCTGCACAGTAG 9

RESULT 699
ADB01850/c
ID ADB01850 standard; DNA; 25 BP.
AC ADB01850;
XX 20-NOV-2003 (first entry)
XX Human MD23 scanning oligonucleotide SEQ ID 2836.
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX Homo sapiens.
XX EPI281758-A2.
XX 05-FEB-2003.
XX 30-JUL-2002; 2002EP-00016874.
XX 02-AUG-2001; 2001US-00922181.
XX (AEOM-) AEOMICA INC.
XX Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX Example 8; SEQ ID NO 2836; 103pp; English.
XX The present invention relates to novel human zinc finger-containing
XX CC proteins and their coding sequences; MD23, MD24, MD27, MD212. MD23 is
XX CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,

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XX CC or in manufacturing a medicament for treating or preventing a disorder
XX CC associated with decreased or increased expression or activity of MD23,
XX CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX CC acids and proteins are also useful for diagnosing or monitoring a disease
XX CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX CC acids can also be used as probes to detect and characterize gross
XX CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX CC useful in constructing microarrays for measuring gene expression. The
XX CC proteins are useful as therapeutic agents for gene therapy or as
XX CC vaccines. The present sequence was used to illustrate the invention.
XX SQ Sequence 25 BP; 7 A; 6 C; 9 G; 3 T; 0 U; 0 Other;

Query Match      22.9%; Score 6.4; DB 1; Length 25;
Best Local Similarity 62.5%; Pred. No. 5.9e+02;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 7 CTACGCTGACAGGAG 22
Db 25 CTCGCTGCACAGTAG 10

RESULT 700
ABI00908
ID ABI00908 standard; DNA; 12 BP.
XX ABI00908;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide primer SEQ ID NO 300881 for detecting SNP TSC0019231.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WC200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 300881; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. The
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

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XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 271278; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 12 BP; 3 A; 4 C; 1 G; 4 T; 0 U; 0 Other;
 Query Match 22.1%; Score 6.2; DB 1; Length 12;
 Best Local Similarity 72.7%; Pred. No. 7e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 3; Gaps 0;
 QY 12 TGTACAGGAG 22
 Db 12 TGTATACGAG 2
 RESULT 704
 ABI37455/C
 ID ABI37455 standard; DNA; 12 BP.
 AC ABI37455;
 XX 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 337428 for detecting SNP TSC0039870.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 XX 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 PF 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 337428; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 12 BP; 3 A; 4 C; 1 G; 4 T; 0 U; 0 Other;
 Query Match 22.1%; Score 6.2; DB 1; Length 12;
 Best Local Similarity 72.7%; Pred. No. 7e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 3; Gaps 0;
 QY 12 TGTACAGGAG 22
 Db 12 TGTATACGAG 2

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 337428; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 22.1%; Score 6.2; DB 1; Length 12;
 Best Local Similarity 72.7%; Pred. No. 7e+02;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 7 CTACGTGTACA 17
 Db 11 CTCCTTCTACA 1
 RESULT 705
 ABI72643
 ID ABI72643 standard; DNA; 12 BP.
 XX ABI72643;
 XX 22-FEB-2002 (first entry)
 DE Oligonucleotide primer SEQ ID NO 372616 for detecting SNP TSC0059501.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 XX 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 PF 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 372616; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 0 Other;
 Query Match 22.1%; Score 6.2; DB 1; Length 12;
 Best Local Similarity 72.7%; Pred. No. 7e+02;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 CTACGCTGAC 17
 Db 2 CTCATATACA 12

RESULT 706
 ABH72448/c
 ID ABH72448 standard; DNA; 12 BP.
 XX AC ABH72448;
 XX AC ABH72448;
 XX DT 22-FEB-2002 (first entry)
 XX DE Oligonucleotide primer SEQ ID NO 272433 for detecting SNP TSC0002816.
 XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX OS WPI; 2001-657177/75.
 XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX PT designed to detect single-nucleotide polymorphisms and cytosine
 XX PT methylation status.
 XX PS Claim 1; SEQ ID NO 272433; 29pp + Sequence Listing; German.
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 0 Other;
 Query Match 22.1%; Score 6.2; DB 1; Length 12;
 Best Local Similarity 72.7%; Pred. No. 7e+02;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 TGTACGGGAG 22

Db 12 TGTATATGAG 2

RESULT 707
 ABI22910/c
 ID ABI22910 standard; DNA; 12 BP.
 XX AC ABI22910;
 XX AC ABI22910;
 XX DT 22-FEB-2002 (first entry)
 XX DE Oligonucleotide primer SEQ ID NO 322883 for detecting SNP TSC0031094.
 XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX OS WPI; 2001-657177/75.
 XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX PT designed to detect single-nucleotide polymorphisms and cytosine
 XX PT methylation status.
 XX PS Claim 1; SEQ ID NO 322883; 29pp + Sequence Listing; German.
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 3 A; 0 C; 8 G; 1 T; 0 U; 0 Other;
 Query Match 22.1%; Score 6.2; DB 1; Length 12;
 Best Local Similarity 72.7%; Pred. No. 7e+02;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 CCTACGCTGAC 16
 Db 12 CCTCCCTCTAC 2

RESULT 708
 ABF18028
 ID ABF18028 standard; DNA; 13 BP.
 XX AC ABF18028;
 XX AC ABF18028;
 XX DT 21-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 118025 for detecting SNP TSC0029509.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 118025; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 0 C; 6 G; 3 T; 0 U; 0 Other;
XX
Query Match 22.1%; Score 6.2; DB 1; Length 13;
Best Local Similarity 72.7%; Pred. No. 7.3e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
Qy 12 TGTACAGGGAG 22
Db 1 TGTAGAAGTAG 11
XX
RESULT 709
ABF18029/c
ID ABF18029 standard; DNA; 13 BP.
XX
AC ABF18029;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 118026 for detecting SNP TSC0029509.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX

PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 118026; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 6 C; 0 G; 4 T; 0 U; 0 Other;
XX
Query Match 22.1%; Score 6.2; DB 1; Length 13;
Best Local Similarity 72.7%; Pred. No. 7.3e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
Qy 12 TGTACAGGGAG 22
Db 13 TGTAGAAGTAG 3
XX
RESULT 710
ABC90236/c
ID ABC90236 standard; DNA; 13 BP.
XX
AC ABC90236;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 90253 for detecting SNP TSC0022616.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 90253; 29pp + Sequence Listing; German.
XX

```

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
  Query Match      22.1%; Score 6.2; DB 1; Length 13;
  Best Local Similarity 72.7%; Pred. No. 7.3e+02;
  Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 13 GTACAGGGAGT 23
Db 12 GTACACGTATT 2
  |||||
  |||||

RESULT 711
ABC90237
ID ABC90237 standard; DNA; 13 BP.
XX
AC ABC90237;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 90254 for detecting SNP TSC0022616.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 90254; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
  Query Match      22.1%; Score 6.2; DB 1; Length 13;
  Best Local Similarity 72.7%; Pred. No. 7.3e+02;
  Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 13 GTACAGGGAGT 23
Db 12 GTACACGTATT 2
  |||||
  |||||

RESULT 711
ABC90237
ID ABC90237 standard; DNA; 13 BP.
XX
AC ABC90237;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 90254 for detecting SNP TSC0022616.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 90254; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
  Query Match      22.1%; Score 6.2; DB 1; Length 13;
  Best Local Similarity 72.7%; Pred. No. 7.3e+02;
  Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 13 GTACAGGGAGT 17
Db 3 CTCACATTACA 13
  |||||
  |||||

RESULT 713

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XX
SQ Sequence 13 BP; 4 A; 3 C; 2 G; 4 T; 0 U; 0 Other;
  Query Match      22.1%; Score 6.2; DB 1; Length 13;
  Best Local Similarity 72.7%; Pred. No. 7.3e+02;
  Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 13 GTACAGGGAGT 23
Db 2 GTACACGTATT 12
  |||||
  |||||

RESULT 712
ABF36729
ID ABF36729 standard; DNA; 13 BP.
XX
AC ABF36729;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 136726 for detecting SNP TSC0034175.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 136726; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 4 C; 0 G; 5 T; 0 U; 0 Other;
  Query Match      22.1%; Score 6.2; DB 1; Length 13;
  Best Local Similarity 72.7%; Pred. No. 7.3e+02;
  Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 7 CTACGTGTACA 17
Db 3 CTCACATTACA 13
  |||||
  |||||

RESULT 713

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ABF60519
 ID ABF60519 standard; DNA; 13 BP.
 AC ABF60519;
 DT 22-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 160516 for detecting SNP TSC0040412.
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 160516; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABH00010-ABH82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 3 A; 6 C; 0 G; 4 T; 0 U; 0 Other;
 XX Query Match 22.1%; Score 6.2; DB 1; Length 13;
 XX Best Local Similarity 72.7%; Pred. No. 7.3e+02;
 XX Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 7 CTACGTGTACA 17
 Db 1 CTCCTTTCTACA 11
 RESULT 714
 ABF60516/c
 ID ABF60516 standard; DNA; 13 BP.
 AC ABF60516;
 XX 22-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 160513 for detecting SNP TSC0040412.
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 160513; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABH00010-ABH82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 5 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
 XX Query Match 22.1%; Score 6.2; DB 1; Length 13;
 XX Best Local Similarity 72.7%; Pred. No. 7.3e+02;
 XX Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 7 CTACGTGTACA 17
 Db 13 CTCCTTTTACA 3
 RESULT 715
 ABC56486
 ID ABC56486 standard; DNA; 13 BP.
 AC ABC56486;
 XX 21-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 56503 for detecting SNP TSC0015314.
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is

XX PT designed to detect single-nucleotide polymorphisms and cytosine

XX PT methylation status.

XX PS Claim 1; SEQ ID NO 56503; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic

XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX CC and cytosine methylation status in chemically pretreated genomic DNA. The

XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX CC range of diseases including immune system, gastrointestinal, respiratory,

XX CC central nervous system, cardiovascular and metabolic disorders. The

XX CC oligomers are also used for detecting cell type differentiation. ABC00010

XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

XX CC represent the oligomers described in the invention. NOTE: The sequence

XX CC data for this patent did not form part of the printed specification, but

XX CC was obtained in electronic format from WIPO at

XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 4 A; 1 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 22.1%; Score 6.2; DB 1; Length 13;

Best Local Similarity 72.7%; Pred. No. 7.3e+02;

Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 13 GTACAGGGAGT 23

Db ||| ||| |||

2 GTRAACGTAGT 12

RESULT 716

ABF82918

ID ABF82918 standard; DNA; 13 BP.

XX AC ABF82918;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 182915 for detecting SNP TSC0045193.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177394-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is

XX PT designed to detect single-nucleotide polymorphisms and cytosine

XX PT methylation status.

XX PS Claim 1; SEQ ID NO 182915; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic

XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX CC and cytosine methylation status in chemically pretreated genomic DNA. The

XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX CC range of diseases including immune system, gastrointestinal, respiratory,

XX CC central nervous system, cardiovascular and metabolic disorders. The

XX CC oligomers are also used for detecting cell type differentiation. ABC00010

XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

XX CC represent the oligomers described in the invention. NOTE: The sequence

XX CC data for this patent did not form part of the printed specification, but

XX CC was obtained in electronic format from WIPO at

XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 3 A; 0 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 22.1%; Score 6.2; DB 1; Length 13;

Best Local Similarity 72.7%; Pred. No. 7.3e+02;

Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 12 TGTACAGGGAG 22

Db ||| ||| |||

2 TGTATATGTAG 12

RESULT 717

ABF36728/c

ID ABF36728 standard; DNA; 13 BP.

XX AC ABF36728;

XX DT 21-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 136725 for detecting SNP TSC0034175.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is

XX PT designed to detect single-nucleotide polymorphisms and cytosine

XX PT methylation status.

XX PS Claim 1; SEQ ID NO 136725; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic

XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX CC and cytosine methylation status in chemically pretreated genomic DNA. The

XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX CC range of diseases including immune system, gastrointestinal, respiratory,

XX CC central nervous system, cardiovascular and metabolic disorders. The

XX CC oligomers are also used for detecting cell type differentiation. ABC00010

XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

XX CC represent the oligomers described in the invention. NOTE: The sequence

XX CC data for this patent did not form part of the printed specification, but

XX CC was obtained in electronic format from WIPO at

XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 5 A; 0 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 22.1%; Score 6.2; DB 1; Length 13;

Best Local Similarity 72.7%; Pred. No. 7.3e+02;

Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 CTACGTTGACA 17
Db 11 CTCATTACA 1

RESULT 718
ABF20036
ID ABF20036 standard; DNA; 13 BP.
XX AC ABF20036;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 120033 for detecting SNP TSC0029958.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX FA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX PS Claim 1; SEQ ID NO 120033; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 6 A; 0 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 22.1%; Score 6.2; DB 1; Length 13;
Best Local Similarity 72.7%; Pred. No. 7.3e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 12 TGTAAGGGAG 22
Db 2 TGTAAGAGTAG 12

RESULT 719
ABF60517
ID ABF60517 standard; DNA; 13 BP.
XX AC ABF60517;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 120034 for detecting SNP TSC0029958.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX WO200177384-A2.
XX PD 18-OCT-2001.

DT 22-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 160514 for detecting SNP TSC0040412.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX FA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX PS Claim 1; SEQ ID NO 160514; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 3 A; 5 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 22.1%; Score 6.2; DB 1; Length 13;
Best Local Similarity 72.7%; Pred. No. 7.3e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 CTACGTTGACA 17
Db 1 CTCCTTTTACA 11

RESULT 720
ABF20037/C
ID ABF20037 standard; DNA; 13 BP.
XX AC ABF20037;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 120034 for detecting SNP TSC0029958.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX WO200177384-A2.
XX PD 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.
 XX
 XX 07-APR-2000; 2000DE-01019173.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 XX
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 120034; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 3 A; 4 C; 0 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 22.1%; Score 6.2; DB 1; Length 13;
 Best Local Similarity 72.7%; Pred. No. 7.3e+02;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 12 TGTACAGGGAG 22
 DB 12 TGTAAAAGTAG 2
 RESULT 721
 ABF60518/c
 ID ABF60518 standard; DNA; 13 BP.
 XX
 XX ABF60518;
 AC
 XX 22-FEB-2002 (first entry)
 DT
 XX Oligonucleotide SEQ ID NO 160515 for detecting SNP TSC0040412.
 DE
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 PN
 XX 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine

PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 160515; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 4 A; 0 C; 6 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 22.1%; Score 6.2; DB 1; Length 13;
 Best Local Similarity 72.7%; Pred. No. 7.3e+02;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 7 CTACGTGTACA 17
 DB 13 CTCCTTCTACA 3
 RESULT 722
 ABC56487/c
 ID ABC56487 standard; DNA; 13 BP.
 XX
 XX ABC56487;
 AC
 XX 21-FEB-2002 (first entry)
 DT
 XX Oligonucleotide SEQ ID NO 56504 for detecting SNP TSC0015314.
 DE
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 PN
 XX 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 56504; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 4 A; 0 C; 6 G; 3 T; 0 U; 0 Other;
 SQ

CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 13 BP; 3 A; 5 C; 1 G; 4 T; 0 U; 0 Other;
 Query Match 22.1%; Score 6.2; DB 1; Length 13;
 Best Local Similarity 72.7%; Pred. No. 7.3e+02;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 13 GTACAGGGAGT 23
 |||||
 Db 12 GTAAAGTACT 2

RESULT 723

ABF82919/C

ID ABF82919 standard; DNA; 13 BP.

AC ABF82919;

XX

DT 22-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 182916 for detecting SNP TSC0045193.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; SS;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

PS Claim 1; SEQ ID NO 182916; 29bp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 13 BP; 6 A; 4 C; 0 G; 3 T; 0 U; 0 Other;
 Query Match 22.1%; Score 6.2; DB 1; Length 13;
 Best Local Similarity 72.7%; Pred. No. 7.3e+02;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 12 TGTACAGGAG 22
 |||||
 Db 12 TGTATATGTAG 2

RESULT 724

AAF46048

ID AAF46048 standard; DNA; 15 BP.

XX

AC AAF46048;

XX

DT 30-MAR-2001 (first entry)

XX

DE IGFBP2 oligonucleotide #887.

XX

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP-2; IGFBP-3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX Homo sapiens.

XX WO200078341-A1.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU000693.

XX 21-JUN-1999; 99US-0140345P.

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wraight CJ, Werther GA, Edmondson SR;

XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

XX Example 6; Page 39; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

XX Sequence 15 BP; 3 A; 8 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 22.1%; Score 6.2; DB 1; Length 15;
 Best Local Similarity 72.7%; Pred. No. 7.7e+02;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 7 CTACGTGTACA 17
 |||||
 Db 2 CTCCTGCACA 12

RESULT 725

AAF46045

ID AAF46045 standard; DNA; 15 BP.
 AC AAF46045;
 XX
 DT 30-MAR-2001 (first entry)
 XX
 DE IGFBP2 oligonucleotide #884.
 XX
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200078341-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 21-JUN-2000; 2000WO-AU000693.
 XX
 PR 21-JUN-1999; 99US-0140345P.
 XX
 PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 PI Wright CJ, Werther GA, Edmondson SR;
 XX
 DR WPI; 2001-041421/05.
 XX
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX
 PS Example 6; Page 39; 201pp; English.
 XX
 CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 3 A; 7 C; 1 G; 4 T; 0 U; 0 Other;
 Query Match 22.1%; Score 6.2; DB 1; Length 15;
 Best Local Similarity 72.7%; Pred. No. 7.7e-02;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 7 CTACGTGTACA 17
 Db |||||
 5 CTCCTGCACA 15
 RESULT 726
 AAF46046
 ID AAF46046 standard; DNA; 15 BP.
 AC AAF46046;
 XX
 DT 30-MAR-2001 (first entry)
 XX
 DE IGFBP2 oligonucleotide #886.
 XX

DT 30-MAR-2001 (first entry)
 XX
 DE IGFBP2 oligonucleotide #885.
 XX
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200078341-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 21-JUN-2000; 2000WO-AU000693.
 XX
 PR 21-JUN-1999; 99US-0140345P.
 XX
 PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 PI Wright CJ, Werther GA, Edmondson SR;
 XX
 DR WPI; 2001-041421/05.
 XX
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX
 PS Example 6; Page 39; 201pp; English.
 XX
 CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 3 A; 7 C; 1 G; 4 T; 0 U; 0 Other;
 Query Match 22.1%; Score 6.2; DB 1; Length 15;
 Best Local Similarity 72.7%; Pred. No. 7.7e-02;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 7 CTACGTGTACA 17
 Db |||||
 4 CTCCTGCACA 14
 RESULT 727
 AAF46047
 ID AAF46047 standard; DNA; 15 BP.
 AC AAF46047;
 XX
 DT 30-MAR-2001 (first entry)
 XX
 DE IGFBP2 oligonucleotide #886.
 XX

KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200078341-A1.
 XX
 PD 28-DEC-2000.
 XX
 XX 21-JUN-2000; 2000WO-AU000693.
 XX
 XX 21-JUN-1999; 99US-0140345P.
 XX
 PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 XX Wright CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 XX
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX
 XX Example 6; Page 39; 201pp; English.
 XX
 CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 3 A; 7 C; 1 G; 4 T; 0 U; 0 Other;
 Query Match 22.1%; Score 6.2; DB 1; Length 15;
 Best Local Similarity 72.7%; Pred. No. 7.7e+02;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 7 CTACGGTGACA 17
 DB |||||
 3 CTCCTGACCA 13
 RESULT 728
 AAT54219/C
 ID AAT54219 standard; RNA; 15 BP.
 AC AAT54219;
 XX
 XX 25-MAR-2003 (revised)
 DT 24-MAR-1997 (first entry)
 XX
 XX Human IL-5 hammerhead ribozyme target sequence (nt. position 91).
 DE
 XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;

KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 ss.
 XX
 XX Homo sapiens.
 OS
 XX
 PN WO9523225-A2.
 XX
 PD 31-AUG-1995.
 XX
 XX 23-FEB-1995; 95WO-IB000156.
 PF
 XX 23-FEB-1994; 94US-00201109.
 PR 29-MAR-1994; 94US-00218934.
 PR 04-APR-1994; 94US-00222795.
 PR 07-APR-1994; 94US-00224483.
 PR 15-APR-1994; 94US-00227958.
 PR 15-APR-1994; 94US-00228041.
 PR 18-MAY-1994; 94US-00245736.
 PR 06-JUL-1994; 94US-00271280.
 PR 15-AUG-1994; 94US-00291932.
 PR 16-AUG-1994; 94US-00291433.
 PR 17-AUG-1994; 94US-00292620.
 PR 19-AUG-1994; 94US-00293520.
 PR 02-SEP-1994; 94US-00300000.
 PR 08-SEP-1994; 94US-00303039.
 PR 23-SEP-1994; 94US-00311486.
 PR 23-SEP-1994; 94US-00311749.
 PR 28-SEP-1994; 94US-00314397.
 PR 03-OCT-1994; 94US-00316771.
 PR 07-OCT-1994; 94US-00319492.
 PR 11-OCT-1994; 94US-00321993.
 PR 04-NOV-1994; 94US-00334847.
 PR 10-NOV-1994; 94US-00337608.
 PR 28-NOV-1994; 94US-00345516.
 PR 16-DEC-1994; 94US-00357577.
 PR 23-DEC-1994; 94US-00363233.
 PR 30-JAN-1995; 95US-00380734.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, McSwiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
 PI Tracz D, Usman N, Wincott PE, Woolf T;
 WPI; 1995-351090/45.
 XX
 DR Ribozymes having modified bases and methods for producing them - for use
 XX in inhibiting disease related genes.
 PT
 XX
 XX Claim 2; Page 214; 407pp; English.
 PS
 XX The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves interleukin-5 (IL-
 CC 5) mRNA at the nucleotide base position indicated in the DE line. Regions
 CC of the mRNA that do not form secondary folding structures and that
 CC contain potential hammerhead and hairpin ribozyme cleavage sites were
 CC identified by computer analysis. Ribozymes directed against these mRNA
 CC sequences were designed and synthesised with modifications that improve
 CC their nuclease resistance. The ribozymes cleave the IL-5 target sequences
 CC and thereby inhibit IL-5 expression, making them useful for treating
 CC chronic asthma, e.g. by inhibiting the synthesis of IL-5 in lymphocytes
 CC and preventing the recruitment and activation of eosinophils. The
 CC ribozymes can also be used to treat eosinophilia (related to parasitic
 CC infection or with pulmonary infiltration) and L-tryptophan-associated
 CC eosinophilia-myalgia syndrome. (Updated on 25-MAR-2003 to correct PI
 CC field.)

```
XX SQ Sequence 15 BP; 2 A; 4 C; 4 G; 0 T; 5 U; 0 Other;
Query Match 22.1%; Score 6.2; DB 1; Length 15;
Best Local Similarity 72.7%; Pred. No. 7.7e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 TACAGGAGTC 24
Db 14 TACACGTAGGC 4

RESULT 729
ADB00349/c
ID ADB00349 standard; DNA; 17 BP.
XX AC ADB00349;
XX DT 20-NOV-2003 (first entry)
XX DE Human MD23 scanning oligonucleotide SEQ ID 1335.
XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 6p21.3-22.2;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX OS Homo sapiens.
XX PN EP1281758-A2.
XX PD 05-FEB-2003.
XX PF 30-JUL-2002; 2002EP-00016874.
XX PR 02-AUG-2001; 2001US-00922181.
XX PA (AEOM-) AEOMICA INC.
XX PI Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX DT New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX PS Example 8; SEQ ID NO 1335; 103pp; English.
XX CC The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX SQ Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 22.1%; Score 6.2; DB 1; Length 17;
Best Local Similarity 72.7%; Pred. No. 7.6e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 TGTACAGGAG 22
Db 12 TGTACAGGAG 22
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```
Db 16 TGCACACGTAG 6

RESULT 730
ADB00350/c
XX ID ADB00350 standard; DNA; 17 BP.
XX AC ADB00350;
XX DT 20-NOV-2003 (first entry)
XX DE Human MD23 scanning oligonucleotide SEQ ID 1336.
XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX OS Homo sapiens.
XX PN EP1281758-A2.
XX PD 05-FEB-2003.
XX PF 30-JUL-2002; 2002EP-00016874.
XX PR 02-AUG-2001; 2001US-00922181.
XX PA (AEOM-) AEOMICA INC.
XX PI Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX DT New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX PS Example 8; SEQ ID NO 1336; 103pp; English.
XX CC The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX SQ Sequence 17 BP; 2 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 22.1%; Score 6.2; DB 1; Length 17;
Best Local Similarity 72.7%; Pred. No. 7.6e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 TGTACAGGAG 22
Db 15 TGCACACGTAG 5

RESULT 731
ADB00352/c
XX ID ADB00352 standard; DNA; 17 BP.
XX
```


XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 1334; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23.
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 22.1%; Score 6.2; DB 1; Length 17;
Best Local Similarity 72.7%; Pred. No. 7.6e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 TGTACAGGGAG 22
DB 17 TGCACACGTAG 7

RESULT 734
ABQ72155
ID ABQ72155 standard; DNA; 9 BP.

XX AC ABQ72155;
XX
XX 28-AUG-2002 (first entry)
XX
XX Zinc finger protein related oligonucleotide target SEQ ID NO:2453.
XX
XX Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.

XX Homo sapiens.
XX Synthetic.

XX WO200242459-A2.

XX 30-MAY-2002.

XX 20-NOV-2001; 2001WO-US043438.

XX 20-NOV-2000; 2000US-00716637.

XX (SANG-) SANGAMO BIOSCIENCES INC.

XX Liu Q;

XX WPI; 2002-500284/53.

XX New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX
XX Example 1; Page 62; 81pp; English.

XX The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subunit. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target subunit, selecting the F2 zinc finger such that it
CC binds to the S2 target subunit, and selecting the F3 zinc finger such
CC that it binds to the S3 target subunit, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target subunits
CC having the nucleotide G in the 5'-most position of the subunit. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention

XX Sequence 9 BP; 1 A; 4 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 21.4%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGCCC 7

DB 3 GGGCCC 8

RESULT 735
ABQ72156
ID ABQ72156 standard; DNA; 9 BP.

XX AC ABQ72156;

XX 28-AUG-2002 (first entry)

XX Zinc finger protein related oligonucleotide target SEQ ID NO:2454.

XX Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.

XX Homo sapiens.

XX Synthetic.

XX WO200242459-A2.

XX 30-MAY-2002.

XX 20-NOV-2001; 2001WO-US043438.

XX 20-NOV-2000; 2000US-00716637.

XX (SANG-) SANGAMO BIOSCIENCES INC.

XX Liu Q;

XX WPI; 2002-500284/53.

XX New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.

XX Example 1; Page 62; 81pp; English.

PS The present invention describes a zinc finger protein (I) that binds to a

CC target site, comprising a first (F1), a second (F2), and a third (F3)

CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the

CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),

CC and a third (S3) target subsequence. Also described are: (i) a polypeptide

CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and

CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it

CC binds to the S1 target subsequence, selecting the F2 zinc finger such that it

CC binds to the S2 target subsequence, and selecting the F3 zinc finger such

CC that it binds to the S3 target subsequence, thus designing (I) that binds to

CC a target site. (I) is useful for recognition of triplet target subsequences

CC having the nucleotide G in the 5'-most position of the subsequence. (I) is

CC useful in studying gene function, and for human therapeutics and plant

CC engineering. (I), (II) or (III) is useful in therapeutic methods to

CC modulate the expression of a target region within a subject, in

CC diagnostic methods for sequence specific detection of target nucleic acid

CC in a sample, and in assays to determine the phenotype and function of

CC gene expression. (I) has improved affinity and specificity for their

CC target sequences, as well as enhanced biological activity. ABQ71213 to

CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc

CC finger peptides which are given in the exemplification of the present

CC invention

SQ Sequence 9 BP; 1 A; 4 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 21.4%; Score 6; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGCCC 7

Db 3 GGGCCC 8

RESULT 736

ADA64482

ID ADA64482 standard; DNA; 9 BP.

AC ADA64482;

XX 20-NOV-2003 (first entry)

DE Zinc finger target sequence DNA #940.

ds; target sequence; zinc finger protein;

multi-finger zinc finger protein; improved affinity;

improved specificity; enhanced biological activity.

Synthetic.

US2003068675-A1.

10-APR-2003.

20-NOV-2001; 2001US-00990186.

24-MAR-1999; 99US-0126238P.

24-MAR-1999; 99US-0126239P.

30-JUL-1999; 99US-0146595P.

30-JUL-1999; 99US-0146615P.

23-MAR-2000; 2000US-00535008.

20-NOV-2000; 2000US-00716637.

(LIUQ/) LIU Q.

Liu Q;

WPI; 2003-567233/53.

Designing zinc finger protein that has three zinc fingers from N-terminus

and C-terminus that bind to subsites in 3' to 5' direction, in a target

site, by selecting zinc fingers that bind their respective subsites.

Disclosure; Page 27; 34pp; English.

The invention relates to a method of designing a zinc finger protein. The

method is useful for designing a zinc finger protein. The method provides

multi-finger zinc finger proteins with improved affinity and specificity

for their target sequences, as well as enhanced biological activity. The

present sequence represents a zinc finger protein DNA target sequence.

Sequence 9 BP; 1 A; 4 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 21.4%; Score 6; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGCCC 7

Db 3 GGGCCC 8

RESULT 737

ADA64483

ID ADA64483 standard; DNA; 9 BP.

AC ADA64483;

XX 20-NOV-2003 (first entry)

DE Zinc finger target sequence DNA #941.

ds; target sequence; zinc finger protein;

multi-finger zinc finger protein; improved affinity;

improved specificity; enhanced biological activity.

Synthetic.

US2003068675-A1.

10-APR-2003.

20-NOV-2001; 2001US-00990186.

24-MAR-1999; 99US-0126238P.

24-MAR-1999; 99US-0126239P.

30-JUL-1999; 99US-0146595P.

30-JUL-1999; 99US-0146615P.

23-MAR-2000; 2000US-00535008.

20-NOV-2000; 2000US-00716637.

(LIUQ/) LIU Q.

Liu Q;

WPI; 2003-567233/53.

Designing zinc finger protein that has three zinc fingers from N-terminus

and C-terminus that bind to subsites in 3' to 5' direction, in a target

site, by selecting zinc fingers that bind their respective subsites.

Disclosure; Page 27; 34pp; English.

The invention relates to a method of designing a zinc finger protein. The

method is useful for designing a zinc finger protein. The method provides

multi-finger zinc finger proteins with improved affinity and specificity

for their target sequences, as well as enhanced biological activity. The

present sequence represents a zinc finger protein DNA target sequence.

Sequence 9 BP; 1 A; 4 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 21.4%; Score 6; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGCCC 7

Db 3 GGGCCC 8

RESULT 738

ADA64484

ID ADA64484 standard; DNA; 9 BP.

AC ADA64484;

XX 20-NOV-2003 (first entry)

DE Zinc finger target sequence DNA #942.

ds; target sequence; zinc finger protein;

multi-finger zinc finger protein; improved affinity;

improved specificity; enhanced biological activity.

Synthetic.

US2003068675-A1.

10-APR-2003.

20-NOV-2001; 2001US-00990186.

24-MAR-1999; 99US-0126238P.

24-MAR-1999; 99US-0126239P.

30-JUL-1999; 99US-0146595P.

30-JUL-1999; 99US-0146615P.

23-MAR-2000; 2000US-00535008.

20-NOV-2000; 2000US-00716637.

(LIUQ/) LIU Q.

Liu Q;

WPI; 2003-567233/53.

Designing zinc finger protein that has three zinc fingers from N-terminus

and C-terminus that bind to subsites in 3' to 5' direction, in a target

site, by selecting zinc fingers that bind their respective subsites.

Disclosure; Page 27; 34pp; English.

The invention relates to a method of designing a zinc finger protein. The

method is useful for designing a zinc finger protein. The method provides

multi-finger zinc finger proteins with improved affinity and specificity

for their target sequences, as well as enhanced biological activity. The

present sequence represents a zinc finger protein DNA target sequence.

Sequence 9 BP; 1 A; 4 C; 4 G; 0 T; 0 U; 0 Other;

PT and C-terminus that bind to subsites in 3' to 5' direction, in a target

PT site, by selecting zinc fingers that bind their respective subsites.

XX Disclosure; Page 27; 34pp; English.

PS The invention relates to a method of designing a zinc finger protein. The

CC method is useful for designing a zinc finger protein. The method provides

CC multi-finger zinc finger proteins with improved affinity and specificity

CC for their target sequences, as well as enhanced biological activity. The

CC present sequence represents a zinc finger protein DNA target sequence.

XX Sequence 9 BP; 1 A; 4 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 21.4%; Score 6; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGCCC 7

Db 3 GGGCCC 8

RESULT 739

ADA64485

ID ADA64485 standard; DNA; 9 BP.

AC ADA64485;

XX 20-NOV-2003 (first entry)

DE Zinc finger target sequence DNA #943.

ds; target sequence; zinc finger protein;

multi-finger zinc finger protein; improved affinity;

improved specificity; enhanced biological activity.

Synthetic.

US2003068675-A1.

10-APR-2003.

20-NOV-2001; 2001US-00990186.

24-MAR-1999; 99US-0126238P.

24-MAR-1999; 99US-0126239P.

30-JUL-1999; 99US-0146595P.

30-JUL-1999; 99US-0146615P.

23-MAR-2000; 2000US-00535008.

20-NOV-2000; 2000US-00716637.

(LIUQ/) LIU Q.

Liu Q;

WPI; 2003-567233/53.

Designing zinc finger protein that has three zinc fingers from N-terminus

and C-terminus that bind to subsites in 3' to 5' direction, in a target

site, by selecting zinc fingers that bind their respective subsites.

Disclosure; Page 27; 34pp; English.

The invention relates to a method of designing a zinc finger protein. The

method is useful for designing a zinc finger protein. The method provides

multi-finger zinc finger proteins with improved affinity and specificity

for their target sequences, as well as enhanced biological activity. The

present sequence represents a zinc finger protein DNA target sequence.

Sequence 9 BP; 1 A; 4 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 21.4%; Score 6; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGCCC 7

Db 3 GGGCCC 8

RESULT 740

ADA64486

ID ADA64486 standard; DNA; 9 BP.

AC ADA64486;

XX 20-NOV-2003 (first entry)

DE Zinc finger target sequence DNA #944.

ds; target sequence; zinc finger protein;

multi-finger zinc finger protein; improved affinity;

improved specificity; enhanced biological activity.

Synthetic.

US2003068675-A1.

10-APR-2003.

20-NOV-2001; 2001US-00990186.

24-MAR-1999; 99US-0126238P.

24-MAR-1999; 99US-0126239P.

30-JUL-1999; 99US-0146595P.

30-JUL-1999; 99US-0146615P.

23-MAR-2000; 2000US-00535008.

20-NOV-2000; 2000US-00716637.

(LIUQ/) LIU Q.

Liu Q;

WPI; 2003-567233/53.

Designing zinc finger protein that has three zinc fingers from N-terminus

and C-terminus that bind to subsites in 3' to 5' direction, in a target

site, by selecting zinc fingers that bind their respective subsites.

Disclosure; Page 27; 34pp; English.

The invention relates to a method of designing a zinc finger protein. The

method is useful for designing a zinc finger protein. The method provides

multi-finger zinc finger proteins with improved affinity and specificity

for their target sequences, as well as enhanced biological activity. The

present sequence represents a zinc finger protein DNA target sequence.

Sequence 9 BP; 1 A; 4 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 21.4%; Score 6; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGCCC 7

Db 3 GGGCCC 8

RESULT 741

ADA64487

ID ADA64487 standard; DNA; 9 BP.

AC ADA64487;

XX 20-NOV-2003 (first entry)

DE Zinc finger target sequence DNA #945.

ds; target sequence; zinc finger protein;

multi-finger zinc finger protein; improved affinity;

improved specificity; enhanced biological activity.

Synthetic.

US2003068675-A1.

10-APR-2003.

20-NOV-2001; 2001US-00990186.

24-MAR-1999; 99US-0126238P.

24-MAR-1999; 99US-0126239P.

30-JUL-1999; 99US-0146595P.

30-JUL-1999; 99US-0146615P.

23-MAR-2000; 2000US-00535008.

20-NOV-2000; 2000US-00716637.

(LIUQ/) LIU Q.

Liu Q;

WPI; 2003-567233/53.

Designing zinc finger protein that has three zinc fingers from N-terminus

and C-terminus that bind to subsites in 3' to 5' direction, in a target

site, by selecting zinc fingers that bind their respective subsites.

Disclosure; Page 27; 34pp; English.

The invention relates to a method of designing a zinc finger protein. The

method is useful for designing a zinc finger protein. The method provides

multi-finger zinc finger proteins with improved affinity and specificity

for their target sequences, as well as enhanced biological activity. The

present sequence represents a zinc finger protein DNA target sequence.

Sequence 9 BP; 1 A; 4 C; 4 G; 0 T; 0 U; 0 Other;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGCCCC 7

Db 3 GGCCCC 8

Search completed: April 19, 2004, 15:00:31
Job time : 4 secs

GenCore version 5.1.6
Copyright (C) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2004, 15:45:29 ; Search time 0.001 Seconds
(without alignments)
202.496 Million cell updates/sec

Title: US-10-024-396-3-COPY

Perfect score: 28

Sequence: 1 cgggcctacgtgtacaggatccagg 28

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 211 seqs, 3616 residues

Total number of hits satisfying chosen parameters: 422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 213 summaries

Database: pmdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	71.4	20	1	PCT-US02-39183-19
C 2	20	71.4	20	1	PCT-US02-39183-20
C 3	20	71.4	20	1	US-10-024-396-19
C 4	20	71.4	20	1	US-10-024-396-20
5	18.6	66.4	25	1	US-09-922-181A-2841
6	18.6	66.4	25	1	US-09-922-181A-2842
7	18.2	65.0	25	1	US-09-922-181A-2839
8	18.2	65.0	25	1	US-09-922-181A-2840
9	17.8	63.6	25	1	US-09-922-181A-2837
10	17.8	63.6	25	1	US-09-922-181A-2838
11	17.8	63.6	25	1	US-09-956-584-315298
12	17.8	63.6	25	1	US-60-234-017-318766
13	17.6	62.9	25	1	US-09-922-181A-2843
14	17.6	62.9	25	1	US-09-954-427A-59195
15	17.2	61.4	25	1	US-09-954-427A-59195
16	17.2	61.4	25	1	US-10-719-900-248399
17	16.8	60.0	25	1	US-60-427-808-248399
18	16.8	60.0	25	1	US-09-922-181A-2836
19	16.6	59.3	25	1	US-09-922-181A-2844
20	16.6	59.3	25	1	US-09-954-427A-108187
21	16.6	59.3	25	1	US-09-954-427A-134734
22	16.6	59.3	25	1	US-09-954-427A-2863
23	16.6	59.3	25	1	US-10-355-577-23855
24	16.6	59.3	25	1	US-10-355-577-23855
25	16.6	59.3	25	1	US-60-234-017-31888
26	16.6	59.3	25	1	US-60-353-987-592056
27	14.4	51.4	17	1	US-09-922-181A-1335
28	14.4	51.4	17	1	PCT-US03-36777-197
29	14.4	51.4	20	1	US-10-713-457-197
30	14.4	51.4	20	1	US-10-714-195-197
31	14.4	51.4	20	1	US-08-983-605-203
32	14.2	50.7	19	1	Sequence 19, Appl
33	14.2	50.7	21	1	Sequence 19, Appl

34	14.2	50.7	21	1	US-09-853-105-19	Sequence 19, Appl
35	13.8	49.3	17	1	US-09-922-181A-1337	Sequence 1337, Ap
36	13.8	49.3	17	1	US-09-922-181A-1338	Sequence 1338, Ap
37	13.8	49.3	17	1	US-09-922-181A-1339	Sequence 1339, Ap
38	13.8	49.3	17	1	US-09-922-181A-1340	Sequence 1340, Ap
39	13.4	47.9	17	1	US-09-922-181A-1334	Sequence 1334, Ap
C 40	13.4	47.9	18	1	US-08-633-792-6	Sequence 6, Appli
C 41	13.4	47.9	18	1	US-08-633-792-6	Sequence 6, Appli
C 42	13.4	47.9	20	1	US-09-918-779-35	Sequence 35, Appl
C 43	13.4	47.9	20	1	US-10-624-932-35	Sequence 35, Appl
44	13.2	47.1	18	1	US-10-310-188-49862	Sequence 49862, A
45	13.2	47.1	19	1	US-10-310-188-49862	Sequence 49862, A
C 46	13.2	47.1	20	1	US-10-159-856-39	Sequence 39, Appl
47	13.2	47.1	20	1	US-10-159-856-105	Sequence 105, App
48	12.8	45.7	17	1	US-09-922-181A-1341	Sequence 1341, Ap
49	12.8	45.7	18	1	US-10-310-188-68257	Sequence 68257, A
50	12.4	44.3	16	1	US-10-316-954-1633	Sequence 1633, Ap
51	12.4	44.3	16	1	US-10-316-954-3538	Sequence 3538, Ap
52	12.4	44.3	17	1	US-09-922-181A-1333	Sequence 1333, Ap
53	12.4	44.3	18	1	US-10-310-188-36260	Sequence 36260, A
54	12.4	44.3	19	1	US-09-356-067-30	Sequence 30, Appl
55	12.4	44.3	19	1	US-10-184-372-23	Sequence 23, Appl
56	12.2	43.6	17	1	US-08-882-945A-275	Sequence 275, App
57	12.2	43.6	17	1	US-09-922-181A-1342	Sequence 1342, Ap
58	12.2	43.6	17	1	US-60-339-764-2159	Sequence 2159, Ap
59	12.2	43.6	17	1	US-60-339-764-2304	Sequence 2304, Ap
C 60	12.2	43.6	18	1	US-10-303-778-16476	Sequence 16476, A
C 61	12	42.9	15	1	PCT-US01-16907-32	Sequence 32, Appl
62	12	42.9	17	1	US-09-922-181A-1331	Sequence 1331, Ap
63	12	42.9	17	1	US-08-922-181A-1332	Sequence 1332, Ap
64	11.8	42.1	16	1	US-08-869-169B-2	Sequence 2, Appli
65	11.8	42.1	16	1	US-09-869-169B-2	Sequence 2, Appli
C 66	11.8	42.1	25	1	US-10-719-900-248399	Sequence 248399
C 67	11.8	42.1	25	1	US-60-427-808-248399	Sequence 248399
68	11.4	40.7	14	1	US-09-555-362-122	Sequence 122, App
C 69	11.4	40.7	15	1	US-10-287-787-6950	Sequence 6950, Ap
C 70	11.4	40.7	15	1	US-10-287-787-20271	Sequence 20271, A
71	11.4	40.7	16	1	US-03-580-522-1	Sequence 1, Appli
C 72	11.4	40.7	17	1	PCT-US02-25943-46322	Sequence 46322, A
C 73	11.4	40.7	17	1	PCT-US02-25943-46323	Sequence 46323, A
C 74	11.4	40.7	17	1	US-09-745-237A-643	Sequence 643, App
C 75	11.4	40.7	17	1	US-09-745-237A-1045	Sequence 1045, Ap
C 76	11.4	40.7	17	1	US-09-745-237A-1120	Sequence 1120, Ap
C 77	11.4	40.7	17	1	US-09-930-423-643	Sequence 643, App
C 78	11.4	40.7	17	1	US-09-930-423-1045	Sequence 1045, Ap
C 79	11.4	40.7	17	1	US-10-227-565-46322	Sequence 46322, Ap
C 80	11.4	40.7	17	1	US-10-227-565-46322	Sequence 46322, A
C 81	11.4	40.7	17	1	US-10-310-188-68063	Sequence 68063, A
82	11.4	40.7	17	1	US-10-310-188-77630	Sequence 77630, A
C 83	11.4	40.7	17	1	US-10-367-832A-46322	Sequence 46322, A
C 84	11.4	40.7	17	1	US-10-367-832A-46323	Sequence 46323, A
C 85	11.4	40.7	17	1	PCT-US02-40948-342	Sequence 342, App
C 86	11.2	40.0	16	1	PCT-US95-03316-23	Sequence 23, Appl
87	11.2	40.0	16	1	PCT-US95-03316-23	Sequence 23, Appl
88	11.2	40.0	16	1	US-08-474-083-23	Sequence 23, Appl
C 89	11.2	40.0	16	1	US-08-474-083-23	Sequence 23, Appl
90	11.2	40.0	16	1	US-08-481-063-23	Sequence 23, Appl
91	11.2	40.0	16	1	US-10-310-188-34900	Sequence 34900, A
92	11.2	40.0	16	1	PCT-US02-16840-1766	Sequence 1766, Ap
93	11.2	40.0	17	1	PCT-US02-16840A-1766	Sequence 1766, Ap
94	11.2	40.0	17	1	US-09-546-745A-6677	Sequence 6677, Ap
95	11.2	40.0	17	1	US-09-818-875-2950	Sequence 2950, Ap
C 96	11.2	40.0	17	1	US-09-818-875-2951	Sequence 2951, Ap
97	11.2	40.0	17	1	US-09-818-875-2951	Sequence 2951, Ap
98	11.2	40.0	17	1	US-09-922-181A-1343	Sequence 1343, Ap
99	11.2	40.0	17	1	US-10-156-306-7025	Sequence 7026, Ap
100	11.2	40.0	17	1	US-10-156-306-7027	Sequence 7027, Ap
C 101	11.2	40.0	17	1	US-10-209-787-2950	Sequence 2950, Ap
102	11.2	40.0	17	1	US-10-209-787-2951	Sequence 2951, Ap
103	11.2	40.0	17	1	US-10-238-700-3087	Sequence 3087, Ap
C 104	11.2	40.0	17	1	US-10-261-185-2950	Sequence 2950, Ap
C 105	11.2	40.0	17	1	US-10-261-185-2951	Sequence 2951, Ap
106	11.2	40.0	17	1	US-10-310-188-41474	Sequence 41474, A

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c 107 11.2 40.0 17 1 US-10-310-188-74621 Sequence 74621, A
c 108 11.2 40.0 17 1 US-10-471-271-2304 Sequence 2304, Ap
c 109 11.2 40.0 17 1 US-10-471-271-2305 Sequence 2305, Ap
c 110 11.2 40.0 17 1 US-10-605-840-2080 Sequence 2080, Ap
c 111 11.2 40.0 17 1 US-10-623-107-2850 Sequence 2850, Ap
c 112 11.2 40.0 17 1 US-10-623-107-2851 Sequence 2851, Ap
c 113 11.2 40.0 17 1 US-10-681-078-2950 Sequence 2950, Ap
c 114 11.2 40.0 17 1 US-10-681-078-2951 Sequence 2951, Ap
c 115 11.2 40.0 17 1 US-10-724-270-1766 Sequence 1766, Ap
c 116 11.2 40.0 17 1 US-10-724-270-1767 Sequence 1767, Ap
c 117 11.2 40.0 17 1 US-60-339-764-2158 Sequence 2158, Ap
c 118 11.2 40.0 17 1 US-60-339-764-2160 Sequence 2160, Ap
c 119 11.2 40.0 17 1 US-60-339-764-2303 Sequence 2303, Ap
c 120 11.2 40.0 17 1 US-60-339-764-2305 Sequence 2305, Ap
c 121 11.2 40.0 17 1 US-10-305-273-941 Sequence 941, Ap
c 122 11.2 40.0 17 1 US-10-305-273-942 Sequence 942, Ap
c 123 11.2 40.0 17 1 US-10-305-275A-941 Sequence 941, Ap
c 124 11.2 40.0 17 1 US-10-305-275A-942 Sequence 942, Ap
c 125 10.8 38.6 16 1 US-10-310-188-56454 Sequence 56454, A
c 126 10.8 38.6 15 1 PCT-US01-44838-5 Sequence 5, Appli
c 127 10.8 38.6 15 1 PCT-US02-25943-41393 Sequence 41393, A
c 128 10.8 38.6 15 1 US-08-774-306-121 Sequence 121, Ap
c 129 10.8 38.6 15 1 US-09-274-553B-143 Sequence 678, Ap
c 130 10.8 38.6 15 1 US-09-274-553B-143 Sequence 143, Ap
c 131 10.8 38.6 15 1 US-09-274-553C-143 Sequence 143, Ap
c 132 10.8 38.6 15 1 US-09-274-553D-143 Sequence 143, Ap
c 133 10.8 38.6 15 1 US-09-274-553E-143 Sequence 143, Ap
c 134 10.8 38.6 15 1 US-09-504-231A-143 Sequence 143, Ap
c 135 10.8 38.6 15 1 US-09-504-231B-143 Sequence 143, Ap
c 136 10.8 38.6 15 1 US-09-611-931-143 Sequence 143, Ap
c 137 10.8 38.6 15 1 US-09-611-931A-143 Sequence 143, Ap
c 138 10.8 38.6 15 1 US-09-633-515-121 Sequence 121, Ap
c 139 10.8 38.6 15 1 US-09-724-389-5 Sequence 5, Appli
c 140 10.8 38.6 15 1 US-10-227-565-41393 Sequence 41393, A
c 141 10.8 38.6 15 1 US-10-367-832A-41393 Sequence 41393, A
c 142 10.4 37.1 12 1 PCT-US03-10286-20 Sequence 34441, A
c 143 10.4 37.1 12 1 US-10-407-637-20 Sequence 20, Appli
c 144 10.4 37.1 12 1 PCT-US01-18815-7 Sequence 7, Appli
c 145 10.4 37.1 15 1 PCT-US01-26215-16 Sequence 16, Appli
c 146 10.4 37.1 15 1 PCT-US01-26488-60 Sequence 60, Appli
c 147 10.4 37.1 15 1 PCT-US01-47434-7 Sequence 7, Appli
c 148 10.4 37.1 15 1 PCT-US02-25940-18950 Sequence 18950, A
c 149 10.4 37.1 15 1 PCT-US02-25942-4864 Sequence 4864, Ap
c 150 10.4 37.1 15 1 PCT-US02-25942-4864 Sequence 4864, Ap
c 151 10.4 37.1 15 1 PCT-US02-25943-22682 Sequence 22682, A
c 152 10.4 37.1 15 1 PCT-US02-25943-34828 Sequence 34828, A
c 153 10.4 37.1 15 1 PCT-US02-25943-37161 Sequence 37161, A
c 154 10.4 37.1 15 1 PCT-US02-25943-48484 Sequence 48484, A
c 155 10.4 37.1 15 1 PCT-US02-25943-62741 Sequence 62741, A
c 156 10.4 37.1 15 1 US-10-227-563-18950 Sequence 18950, A
c 157 10.4 37.1 15 1 US-10-227-563-34828 Sequence 34828, A
c 158 10.4 37.1 15 1 US-10-227-563-37161 Sequence 37161, A
c 159 10.4 37.1 15 1 US-10-227-563-48484 Sequence 48484, A
c 160 10.4 37.1 15 1 US-10-227-563-62741 Sequence 62741, A
c 161 10.4 37.1 15 1 US-10-227-565-4864 Sequence 4864, Ap
c 162 10.4 37.1 15 1 US-10-227-567-4864 Sequence 4864, Ap
c 163 10.4 37.1 15 1 US-10-227-567-6581 Sequence 6581, Ap
c 164 10.4 37.1 15 1 US-10-227-567-72958 Sequence 27958, A
c 165 10.4 37.1 15 1 US-10-227-729A-4864 Sequence 4864, Ap
c 166 10.4 37.1 15 1 US-10-367-832A-6581 Sequence 6581, Ap
c 167 10.4 37.1 15 1 US-10-367-832A-22682 Sequence 22682, A
c 168 10.4 37.1 15 1 US-10-367-832A-34828 Sequence 34828, A
c 169 10.4 37.1 15 1 US-10-367-832A-37161 Sequence 37161, A
c 170 10.4 37.1 15 1 US-10-367-832A-48484 Sequence 48484, A
c 171 10.4 37.1 15 1 US-10-367-832A-62741 Sequence 62741, A
c 172 10.4 37.1 15 1 US-10-367-892-18950 Sequence 18950, A
c 173 10.4 37.1 16 1 PCT-US02-25943-33165 Sequence 33165, A
c 174 10.4 37.1 16 1 PCT-US02-25943-33166 Sequence 33166, A
c 175 10.4 37.1 16 1 PCT-US02-25943-34829 Sequence 34829, A
c 176 10.4 37.1 16 1 US-10-227-565-33165 Sequence 33165, A
c 177 10.4 37.1 16 1 US-10-227-565-33166 Sequence 33166, A
c 178 10.4 37.1 16 1 US-10-227-565-34829 Sequence 34829, A
c 179 10.4 37.1 16 1 US-10-305-274-517 Sequence 517, Ap

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16 1 US-10-305-274-1406 Sequence 1406, Ap
16 1 US-10-367-832A-33165 Sequence 33165, A
16 1 US-10-367-832A-33166 Sequence 33166, A
16 1 US-10-367-832A-34829 Sequence 34829, A
16 1 PCT-US02-25940-12401 Sequence 12401, A
15 1 PCT-US02-25940-14568 Sequence 14568, A
15 1 PCT-US02-25943-27773 Sequence 27773, A
15 1 PCT-US02-25943-31162 Sequence 31162, A
15 1 PCT-US02-25943-31163 Sequence 31163, A
15 1 US-09-406-643-897 Sequence 897, Ap
15 1 US-09-408-824A-897 Sequence 897, Ap
15 1 US-09-611-577-21 Sequence 21, Appli
15 1 US-09-679-813-73 Sequence 73, Appli
15 1 US-09-912-673A-55 Sequence 55, Appli
15 1 US-10-146-505-73 Sequence 73, Appli
15 1 US-10-227-563-12401 Sequence 12401, A
15 1 US-10-227-563-14568 Sequence 14568, A
15 1 US-10-227-565-6183 Sequence 6183, Ap
15 1 US-10-227-565-27773 Sequence 27773, A
15 1 US-10-227-565-31162 Sequence 31162, A
15 1 US-10-227-565-31163 Sequence 31163, A
15 1 US-10-287-787-16396 Sequence 16396, A
15 1 US-10-287-787-16397 Sequence 16397, A
15 1 US-10-287-787-22102 Sequence 22102, A
15 1 US-10-310-188-22105 Sequence 22105, A
15 1 US-10-367-832A-27773 Sequence 27773, A
15 1 US-10-367-832A-31162 Sequence 31162, A
15 1 US-10-367-832A-31163 Sequence 31163, A
15 1 US-10-367-892-12401 Sequence 12401, A
15 1 US-10-367-892-14568 Sequence 14568, A
15 1 US-10-453-850-897 Sequence 897, Ap

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ALIGNMENTS

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RESULT 1
PCT-US02-39183-19/c
; Sequence 19, Application PC/TUS0239183
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Isis Pharmaceuticals, Inc.
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD3611 EXPRESSION
; FILE REFERENCE: RTSP-0453
; CURRENT APPLICATION NUMBER: PCT/US02/39183
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 10/024,396
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US02-39183-19

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Query Match 71.4%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CGGGCCCTACGTGTACAGG 20
    |||||
Db 20 CGGGCCCTACGTGTACAGG 1

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RESULT 2
PCT-US02-39183-20/c
; Sequence 20, Application PC/TUS0239183
; GENERAL INFORMATION:

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; APPLICANT: Kenneth W. Dobie
; APPLICANT: Isis Pharmaceuticals, Inc.
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD3611 EXPRESSION
; FILE REFERENCE: RTSF-0453
; CURRENT APPLICATION NUMBER: PCT/US02/39183
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 10/024,396
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US02-39183-20

Query Match      71.4%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 ACGTGTACAGGAGTCCAGG 28
Db      20 ACGTGTACAGGAGTCCAGG 1

RESULT 3
US-10-024-396-19/c
; Sequence 19, Application US/10024396
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD3611 EXPRESSION
; FILE REFERENCE: RTS-0339
; CURRENT APPLICATION NUMBER: US/10/024,396
; CURRENT FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-024-396-19

Query Match      71.4%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGGGCCCTACGTGTACAGG 20
Db      20 CGGGCCCTACGTGTACAGG 1

RESULT 4
US-10-024-396-20/c
; Sequence 20, Application US/10024396
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD3611 EXPRESSION
; FILE REFERENCE: RTS-0339
; CURRENT APPLICATION NUMBER: US/10/024,396
; CURRENT FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-024-396-20

Query Match      71.4%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 ACGTGTACAGGAGTCCAGG 28
Db      20 ACGTGTACAGGAGTCCAGG 1

PCT-US02-39183-20

; APPLICANT: Kenneth W. Dobie
; APPLICANT: Isis Pharmaceuticals, Inc.
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD3611 EXPRESSION
; FILE REFERENCE: RTSF-0453
; CURRENT APPLICATION NUMBER: PCT/US02/39183
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 10/024,396
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
PCT-US02-39183-20

Query Match      71.4%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 ACGTGTACAGGAGTCCAGG 28
Db      20 ACGTGTACAGGAGTCCAGG 1

RESULT 5
US-09-922-181A-2841
; Sequence 2841, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AN
; FILE REFERENCE: AEOMICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2841
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-2841

Query Match      66.4%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      3 GGCCTACGTGTACAGGAGTCCAG 27
Db      1 GGCCTACGTGTACAGGAGTCCAG 25

RESULT 6
US-09-922-181A-2842
; Sequence 2842, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AN
; FILE REFERENCE: AEOMICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2842
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-2842

Query Match      66.4%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      4 GGCCTACGTGTACAGGAGTCCAGG 28
Db      1 GGCCTACGTGTACAGGAGTCCAGG 25

RESULT 7
US-09-922-181A-2839
; Sequence 2839, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AN
; FILE REFERENCE: AEOMICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
```

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; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2839
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-2839

Query Match      65.0%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGCCTACGTGTACAGGAGTCC 25
   |||||
Db 3 GGCCTACGTGTACAGGAGTCC 25

RESULT 8
US-09-922-181A-2840
; Sequence 2840, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AND
; FILE REFERENCE: AEMICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2840
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-2840

Query Match      65.0%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGCCTACGTGTACAGGAGTCC 25
   |||||
Db 2 GGCCTACGTGTACAGGAGTCC 24

RESULT 9
US-09-922-181A-2837
; Sequence 2837, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AND
; FILE REFERENCE: AEMICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2837
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-2837

Query Match      63.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCTACGTGTACAGGAGT 23
   |||||
Db 5 GGCCTACGTGTACAGGAGT 25

RESULT 10
US-09-922-181A-2838
; Sequence 2838, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AND
; FILE REFERENCE: AEMICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2838
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-2838

Query Match      63.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCTACGTGTACAGGAGT 23
   |||||
Db 4 GGCCTACGTGTACAGGAGT 24

RESULT 11
US-09-956-584-315298
; Sequence 315298, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 315298
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-315298

Query Match      63.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGCCTACGTGTACAGGAGTC 24
   |||||
Db 3 GGCCTACGTGTACAGGAGTC 23

RESULT 12
US-60-234-017-318766
; Sequence 318766, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Mittman, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 318766
; LENGTH: 25
; TYPE: DNA
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; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AW123720
US-60-234-017-318766

Query Match      63.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGCCTACGTGTACAGGAGTC 24
   ||||| ||||| ||||| |||||
Db 3 GCCTGTGTGTACAGGAGTC 23

RESULT 13
US-09-922-181A-2843
; Sequence 2843, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AND
; FILE REFERENCE: AEOMICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2843
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-2843

Query Match      62.9%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 CCCTACGTGTACAGGAGTCACGG 28
   ||||| ||||| ||||| |||||
Db 1 CCCTACGTGTGCAGCGAGTGCTGG 24

RESULT 14
US-09-954-427A-59195
; Sequence 59195, Application US/09954427A
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat Genome
; FILE REFERENCE: 3112.1
; CURRENT APPLICATION NUMBER: US/09/954,427A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,166
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 59195
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus Norvegicus
US-09-954-427A-59195

Query Match      62.9%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GGCCTACGTGTACAGGAGTCACCA 26
   ||||| ||||| ||||| |||||
Db 2 GTCCCAAGTGTGCAGGAGTCACCA 25

RESULT 15
US-10-719-900-248399
; Sequence 248399, Application US/10719900
```

```
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 248399
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-248399

Query Match      61.4%; Score 17.2; DB 1; Length 25;
Best Local Similarity 86.4%; Pred. No. 23;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGGAGTCCAGG 28
   ||||| ||||| ||||| |||||
Db 3 CTCCTGTACAGGAGTCCAGG 24

RESULT 16
US-60-427-808-248399
; Sequence 248399, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 248399
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-248399

Query Match      61.4%; Score 17.2; DB 1; Length 25;
Best Local Similarity 86.4%; Pred. No. 23;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGGAGTCCAGG 28
   ||||| ||||| ||||| |||||
Db 3 CTCCTGTACAGGAGTCCAGG 24

RESULT 17
US-09-922-181A-2836
; Sequence 2836, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AN
; FILE REFERENCE: AEOMICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2836
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-2836

Query Match      60.0%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 134734
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus Norvegicus
US-09-954-427A-134734

```

```

Query Match      59.3%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred.No. 28;
Matches 19; Conservative 0; Mismatches 4; Indels

Qy      3  GGCCCTACGTTGACGGGAGTCC 25
          |||||
Db      2  GGCCCTACGTTGCGGAGATGC 24

```

```

RESULT 21
US-09-956-584-2663
; Sequence 2663, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 2663
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-2663

```

	Query Match	59.3%	Score 16.6	DB 1	Length 25
	Best Local Similarity	82.6% <td></td> <td></td> <td></td>			
	Matches	19	Conservative	0	Mismatches 4
QY		6	CCTACGTTACAGGGAGTCCAGG	28	
NP		2	CCTAAGTTCACAGGGAGTCCCGG	24	

```

RESULT 22
US-10-355-577-23855
; Sequence 23855, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-UI33
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 23855
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-23855

```

	Query Match	59.3%	Score 16.6;	DB 1;	Length 25;
	Best Local Similarity	82.6%;	Fred. No. 28;		
	Matches 19; Conservative	0;	Mismatches	4; Indels	0; Gaps
Qy	6 CCTACGTGTACAGGGAGTCCAGG	28			
Dd	3 CCCACGTGTACAGGGGGTTCCGG	25			

RESULT 23
US-10-355-577-592056/c

```

Qy      3  GGCCCTACGTGTACAGGAG  22
      |||||
Db      6  GGCCCTACGTGTGCACGAG  25
      |||||

RESULT 18
US-C9-922-181A-2844
; Sequence 2844 Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, fizhong
; APPLICANT: Shannon, Mark
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AND
; FILE REFERENCE: AEOICA-12
; CURRENT APPLICATION NUMBER: US/09/922.181A
; CURRENT FILING DATE: 2001-12-12

```

```

; CURRENT FILING DATE: 2001-12-12
;
; NUMBER OF SEQ ID NOS: 7046
;
; SOFTWARE: Aeonica Sequence Listing Engine
;
; SEQ ID NO 2844
;
; LENGTH: 25
;
; TYPE: DNA
;
; ORGANISM: Homo sapiens
;
US-09-922-181A-2844

```

Query Match	59.3%	Score 16.6;	DB 1;	Length 25;
Best Local Similarity	82.6%	Pred. No. 28;		
Matches 19;	Conservative	0;	Mismatches 4;	Indels 0;
				Gaps 0;

QY
6 CCTACGTGTACAGGGAGTCCAGG 28
|||
1 CCTACGTGTGCAGCGAGTGCTGG 23
db

```

RESULT 19
US-09-954-427A-108187/c
; Sequence 108187, Application US/09954427A
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat Genome
; FILE REFERENCE: 3112.1
; CURRENT APPLICATION NUMBER: US/09/954,427A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,166
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 108187
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus Norvegicus
US-09-954-427A-108187

```

Query Match 59.3%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGGCCCTACGTGTACAGGAGTC 24
24 GCGCTCTACGTGGACAGTGAGTC 2
Db

```

RESULT 20
US-09-954-427A-134734
; Sequence 134734, Application US/09954427A
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat Genome
; FILE REFERENCE: 3112.1
; CURRENT APPLICATION NUMBER: US/09/954.427A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,166
; PRIOR FILING DATE: 2000-09-18

```

```

; Sequence 592056, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 592056
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-592056

Query Match          59.3%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 CCTACGTGTACAGGGAGTCCAGG 28
Db 3 CCCACGTGTACAGGGGGTTCGG 25

RESULT 26
US-60-353-987-592056/c
; Sequence 592056, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 592056
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-592056

Query Match          59.3%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 CCTACGTGTACAGGGAGTCCAGG 28
Db 24 CCTACGTGTCTAGGGACACCAGG 2

RESULT 27
US-09-922-181A-1335
; Sequence 1335, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 ANI
; FILE REFERENCE: AECOMICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1335
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-1335

Query Match          51.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 25;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGCCTACGTGTACAG 18
Db 2 GGCCTACGTGTGCAG 17

RESULT 28
US-09-922-181A-1336
; Sequence 1336, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 ANI
; FILE REFERENCE: AECOMICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1336
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-1336

Query Match          59.3%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 CCTACGTGTACAGGGAGTCCAGG 28
Db 24 CCTACGTGTCTAGGGACACCAGG 2

RESULT 24
US-60-234-017-31888
; Sequence 31888, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Mittmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31888
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AV359510
US-60-234-017-31888

Query Match          59.3%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 CCTACGTGTACAGGGAGTCCAGG 28
Db 2 CCTACGTGTACAGGGAGTCCCG 24

RESULT 25
US-60-353-987-23855
; Sequence 23855, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 23855
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-23855

Query Match          59.3%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 CCTACGTGTACAGGGAGTCCAGG 28
Db 2 CCTACGTGTCTAGGGACACCAGG 2

```

```
/ SOFTWARE: Aeomica Sequence Listing Engine
/ SEQ ID NO 1336
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-922-181A-1336

Query Match          51.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 25;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGCCCTACGTGTACAG 18
Db 1 GGCCCTACGTGTCCAG 15

RESULT 29
PCT-US03-36777-197/c
/ Sequence 197, Application PC/TUS0336777
/ GENERAL INFORMATION:
/ APPLICANT: Genomic Health
/ APPLICANT: Vall d' Hebron University Hostipal
/ APPLICANT: Baker, Joffre
/ APPLICANT: Cronin, Maureen
/ APPLICANT: Shak, Steve
/ APPLICANT: Baselga, Jose
/ TITLE OF INVENTION: GENE EXPRESSION PROFILING OF EGFR
/ FILE REFERENCE: 39740-0005
/ CURRENT APPLICATION NUMBER: PCT/US03/36777
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/427090
/ NUMBER OF SEQ ID NOS: 372
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 197
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: primer
PCT-US03-36777-197

Query Match          51.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 37;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CCTACGTGTACAGGA 21
Db 20 CCTACGGGTACAGGA 5

RESULT 30
US-10-713-457-197/c
/ Sequence 197, Application US/10713457
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Joffre
/ APPLICANT: Cronin, Maureen
/ APPLICANT: Shak, Steve
/ APPLICANT: Baselga, Jose
/ TITLE OF INVENTION: GENE EXPRESSION PROFILING OF EGFR
/ FILE REFERENCE: 39740-0005
/ CURRENT APPLICATION NUMBER: US/10/713,457
/ PRIOR FILING DATE: 2003-11-13
/ PRIOR APPLICATION NUMBER: 60/427090
/ NUMBER OF SEQ ID NOS: 372
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 197
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence

Query Match          51.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 37;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CCTACGTGTACAGGA 21
Db 20 CCTACGGGTACAGGA 5

RESULT 31
US-10-714-195-197/c
/ Sequence 197, Application US/10714195
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Joffre
/ APPLICANT: Cronin, Maureen
/ APPLICANT: Shak, Steve
/ APPLICANT: Baselga, Jose
/ TITLE OF INVENTION: GENE EXPRESSION PROFILING OF EGFR
/ FILE REFERENCE: 39740-0005
/ CURRENT APPLICATION NUMBER: US/10/714,195
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/427090
/ NUMBER OF SEQ ID NOS: 372
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 197
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: primer
US-10-714-195-197

Query Match          51.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 37;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CCTACGTGTACAGGA 21
Db 20 CCTACGGGTACAGGA 5

RESULT 32
US-08-983-605-203/c
/ Sequence 203, Application US/08983605A
/ GENERAL INFORMATION:
/ APPLICANT: Roder, Marion
/ TITLE OF INVENTION: Microsatellite Markers for Plants of the Species
/ TITLE OF INVENTION: Triticum Aestivum and Tribe Triticeae and the Use of
/ FILE REFERENCE: 2936.10400
/ CURRENT APPLICATION NUMBER: US/08/983,605A
/ CURRENT FILING DATE: 1998-05-01
/ EARLIER APPLICATION NUMBER: DE 195 25 284.5
/ PRIOR FILING DATE: 1995-06-28
/ NUMBER OF SEQ ID NOS: 466
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 203
/ LENGTH: 19
/ TYPE: DNA
/ ORGANISM: Triticum aestivum
US-08-983-605-203

Query Match          50.7%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 35;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCCTACGTGTACAGGAG 22
```



```
; FILE REFERENCE: AEOMICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1338
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-1338

Query Match      49.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 31;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCTACGTGTACAGGGA 21
   |||||
Db 1 CCTACGTGTACAGGGA 17

RESULT 37
US-09-922-181A-1339
; Sequence 1339, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AND
; FILE REFERENCE: AEOMICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1339
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-1339

Query Match      49.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 31;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCTACGTGTACAGGAG 22
   |||||
Db 1 CCTACGTGTACAGGAG 17

RESULT 38
US-09-922-181A-1340
; Sequence 1340, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AND
; FILE REFERENCE: AEOMICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1340
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-1340

Query Match      49.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 31;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGGAGT 23
   |||||
Db 1 CTACGTGTACAGGAGT 17

RESULT 39
US-09-922-181A-1334
; Sequence 1334, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AND
; FILE REFERENCE: AEOMICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1334
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-1334

Query Match      47.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 36;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGTACA 17
   |||||
Db 3 GGCCCTACGTGTGCA 17

RESULT 40
US-08-633-792-6/c
; Sequence 6, Application US/08633792
; GENERAL INFORMATION:
; APPLICANT: Barrett, Graham L
; TITLE OF INVENTION: A METHOD FOR ENHANCING NEURONE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,792
; FILING DATE: 01-JUL-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PM/1870
; FILING DATE: 18-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516)742-4366
; TELEFAX: (516)742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA oligonucleotide"
```

US-08-633-792-6

Query Match 47.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 42;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 TGTACAGGAGTCCA 26
|||||
Db 17 TGTACAGGAGTCCA 3

RESULT 41

US-09-075-717-6/c
; Sequence 6, Application US/09075717
; GENERAL INFORMATION:
; APPLICANT: Barrett, Graham L
; TITLE OF INVENTION: A METHOD FOR ENHANCING NEURONE SURVIVAL
; TITLE OF INVENTION: AND AGENTS USEFUL FOR SAME
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/075,717
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/633,792
; FILING DATE: 01-JUL-1996
; APPLICATION NUMBER: AU PM/1870
; FILING DATE: 18-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516)742-4343
; TELEFAX: (516)742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA oligonucleotide"

US-09-075-717-6

Query Match 47.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 42;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 TGTACAGGAGTCCA 26
|||||
Db 17 TGTACAGGAGTCCA 3

RESULT 42

US-09-918-779-35/c
; Sequence 35, Application US/09918779
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shinkets, Richard
; APPLICANT: Zernusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alsbrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/09/918,779
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,762
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,770
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,769
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/225,146
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,392
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,470
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,697
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/263,662
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/281,645
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Oligonucleotide
; OTHER INFORMATION: primers
; OTHER INFORMATION: primers
US-09-918-779-35

Query Match 47.9%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 54;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 TACAGGAGTCCAGG 28
|||||
Db 17 TACAGGAGTCCAGG 3

RESULT 43

US-10-624-932-35/c
; Sequence 35, Application US/10624932
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven

```

; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-57779

Query Match 47.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 45;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 ACGTGTCAGGAGTCCA 26
   ||| ||||| |||
Db 1 ACGGTACAGGAGGTCA 18

RESULT 45
US-10-310-188-49862
; Sequence 49862, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49862
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-49862

Query Match 47.1%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 51;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 11 GTGTACAGGAGTCCAG 28
   ||| ||||| |||||
Db 2 GTGTACAGGAGTCCAG 19

RESULT 46
US-10-159-856-39/c
; Sequence 39, Application US/10159856
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPRESSION
; FILE REFERENCE: RTS-0365
; CURRENT APPLICATION NUMBER: US/10/159,856
; CURRENT FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 134
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-159-856-39

Query Match 47.1%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCCCTACGTTACAGGA 21
   ||| ||||| |||||
Db 19 GCGCATCGTGTACAGGA 2

RESULT 47
US-10-159-856-105
; Sequence 105, Application US/10159856
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57779

```

APPLICANT: Susan M. Freier
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPRE
FILE REFERENCE: RTS-0365
CURRENT APPLICATION NUMBER: US/10/159,856
CURRENT FILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 134
SEQ ID NO 105
LENGTH: 20
TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
US-10-159-856-105

Query Match 47.1%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCCTACGTGTACAGGA 21
||| |||||
Db 2 GCGCATCGTGTACAGGA 19

RESULT 48
US-09-922-181A-1341
GENERAL INFORMATION:
APPLICANT: Gu, Yizhong
APPLICANT: Shannon, Mark
APPLICANT: Nguyen, Cung-Tuong
TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MDZ3, MDZ4, MDZ7 AND
FILE REFERENCE: AEOmica-12
CURRENT APPLICATION NUMBER: US/09/922,181A
CURRENT FILING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 7046
SOFTWARE: AeoMica Sequence Listing Engine
SEQ ID NO 1341
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-922-181A-1341

Query Match 45.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 TACGTGTACAGGAGT 23
||| |||||
Db 1 TACGTGTACAGGAGT 16

RESULT 49
US-10-310-188-68257
GENERAL INFORMATION:
APPLICANT: RosettaGenomics
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PatentIn version 3.1
SEQ ID NO 68257
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
US-10-310-188-68257

Query Match 45.7%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 52;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 GTACAGGGAGTCCAGG 28
||| |||||
Db 1 GAAAGGGAGTCCAGG 16

RESULT 50
US-10-316-954-1633
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Escherichia coli O157:H7, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/316,954
CURRENT FILING DATE: 2002-12-12
NUMBER OF SEQ ID NOS: 5998
SOFTWARE: Proprietary
SEQ ID NO 1633
LENGTH: 16
TYPE: DNA
ORGANISM: Escherichia coli O157:H7, complete genome.
FEATURE:
LOCATION: (1432166)...(1432181)
OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 20
US-10-316-954-1633

Query Match 44.3%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 46;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGGAGTCCAGG 28
||| |||||
Db 3 ACAGGGAGTACAGG 16

RESULT 51
US-10-316-954-3538/c
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Escherichia coli O157:H7, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/316,954
CURRENT FILING DATE: 2002-12-12
NUMBER OF SEQ ID NOS: 5998
SOFTWARE: Proprietary
SEQ ID NO 3538
LENGTH: 16
TYPE: DNA
ORGANISM: Escherichia coli O157:H7, complete genome.
FEATURE:
LOCATION: (2694503)...(2694518)
OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 44
US-10-316-954-3538

Query Match 44.3%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 46;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGGAGTCCAGG 28
||| |||||
Db 14 ACAGGGAGTACAGG 1

RESULT 52
US-09-922-181A-1333
GENERAL INFORMATION:
APPLICANT: Gu, Yizhong
APPLICANT: Shannon, Mark
APPLICANT: Nguyen, Cung-Tuong
TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MDZ3, MDZ4, MDZ7 AND
FILE REFERENCE: AEOmica-12
CURRENT APPLICATION NUMBER: US/09/922,181A

```
/ CURRENT FILING DATE: 2001-12-12
/ NUMBER OF SEQ ID NOS: 7046
/ SOFTWARE: Aecomica Sequence Listing Engine
/ SEQ ID NO 1333
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-922-181A-1333

Query Match      44.3%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 53;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGCCTACGTGAC 16
   |||||
Db 4 GGCCTACGTGTC 17

RESULT 53
US-10-310-188-36260
/ Sequence 36260, Application US/10310188
/ GENERAL INFORMATION:
/ APPLICANT: RosettaGenomics
/ TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
/ FILE REFERENCE: 47487
/ CURRENT APPLICATION NUMBER: US/10/310,188
/ CURRENT FILING DATE: 2002-12-19
/ NUMBER OF SEQ ID NOS: 86841
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 36260
/ LENGTH: 18
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-310-188-36260

Query Match      44.3%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 61;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGG 20
   |||||
Db 2 CTACGTGTACAGG 15

RESULT 54
US-09-356-067-30
/ Sequence 30, Application US/09356067
/ GENERAL INFORMATION:
/ APPLICANT: North, Michael
/ APPLICANT: Nishina, Patsy
/ APPLICANT: Naggart, Juergen
/ APPLICANT: Noben-Trauth, Konrad
/ TITLE OF INVENTION: GENE FAMILY ASSOCIATED WITH
/ NUMBER OF SEQUENCES: 67
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Bozicevic & Reed, LLP
/ STREET: 285 Hamilton Avenue, Suite 200
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94301
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FASTSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/356,067
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:

/ CURRENT FILING DATE: 2001-12-12
/ NUMBER OF SEQ ID NOS: 7046
/ SOFTWARE: Aecomica Sequence Listing Engine
/ SEQ ID NO 1333
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-922-181A-1333

APPLICATION NUMBER: 09/032,365
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEQ-2CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
TELEFAX: 650-327-3231
TELEX:
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-356-067-30

Query Match      44.3%; Score 12.4; DB 1; Length 19;
Best Local Similarity 92.9%; Pred. No. 69;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGAGTCCAGG 28
   |||||
Db 6 ACAGGAGACCAGG 19

RESULT 55
US-10-184-372-23
/ Sequence 23, Application US/10184372
/ GENERAL INFORMATION:
/ APPLICANT: Bank, Rudolf A.
/ APPLICANT: Van der Slot, Annemarie J.
/ APPLICANT: Zuurmond, Anne-Marie
/ APPLICANT: Te Koppele, Johannes M.
/ TITLE OF INVENTION: Modification of collagenous materials and medical treatment, di
/ FILE REFERENCE: P60187US00
/ CURRENT APPLICATION NUMBER: US/10/184,372
/ CURRENT FILING DATE: 2003-06-19
/ PRIOR APPLICATION NUMBER: US 09/450,209
/ PRIOR FILING DATE: 1999-11-29
/ NUMBER OF SEQ ID NOS: 59
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 23
/ LENGTH: 19
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: primer
US-10-184-372-23

Query Match      44.3%; Score 12.4; DB 1; Length 19;
Best Local Similarity 92.9%; Pred. No. 69;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGAGTCCAGG 28
   |||||
Db 3 ACAGGAGTCCAGG 16

RESULT 56
US-09-882-945A-275
/ Sequence 275, Application US/09882945A
/ GENERAL INFORMATION:
/ APPLICANT: Lyamichev, Victor
/ APPLICANT: Allawi, Hatim
/ APPLICANT: Dong, Fang
/ APPLICANT: Neri, Bruce
/ APPLICANT: Vener, Tatiana
/ TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
/ FILE REFERENCE: FORS-04586
```



```
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-16907-32

Query Match          42.9%; Score 12; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 45;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 CCGTACAGGGAGT 23
Db 1 CCGTACAGGGAGY 14

RESULT 62
US-09-922-181A-1331
; Sequence 1331, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AND
; FILE REFERENCE: AEOMICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1331
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-1331

Query Match          42.9%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGT 14
Db 6 GGCCCTACGTGT 17

RESULT 63
US-09-922-181A-1332
; Sequence 1332, Application US/09922181A
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AND
; FILE REFERENCE: AEOMICA-12
; CURRENT APPLICATION NUMBER: US/09/922,181A
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1332
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-1332

Query Match          42.9%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGT 14
Db 5 GGCCCTACGTGT 16

RESULT 64
US-09-869-169-2
; Sequence 2, Application US/09869169
; GENERAL INFORMATION:
; APPLICANT: Paulussen, Aimee
; APPLICANT: Armstrong, Martin
; TITLE OF INVENTION: Genotyping Cytochrome Expression
; FILE REFERENCE: 51639/001
; CURRENT APPLICATION NUMBER: US/09/869,169
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: GB 9828619.8
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-869-169-2

Query Match          42.1%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 57;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 GTACAGGGAGTCCAG 27
Db 2 GTACAGGGAGCACAG 16

RESULT 65
US-09-869-169B-2
; Sequence 2, Application US/09869169B
; GENERAL INFORMATION:
; APPLICANT: Paulussen, Aimee
; APPLICANT: Armstrong, Martin
; TITLE OF INVENTION: Genotyping Cytochrome Expression
; FILE REFERENCE: 51639/001
; CURRENT APPLICATION NUMBER: US/09/869,169B
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: GB 9828619.8
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-869-169B-2

Query Match          42.1%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 57;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 GTACAGGGAGTCCAG 27
Db 2 GTACAGGGAGCACAG 16

RESULT 66
US-10-719-900-248399/c
; Sequence 248399, Application US/10719900
; GENERAL INFORMATION:
; APPLICANT: Xue Wei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 248399
; LENGTH: 25
```



```
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-248399

Query Match      42.1%; Score 11.8; DB 1; Length 25;
Best Local Similarity 86.7%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      8 TACGGGTACAGGAG 22
Db      17 TCCTGTACAGGAG 3

RESULT 67
US-60-427-808-248399/c
; Sequence 248399, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 248399
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-248399

Query Match      42.1%; Score 11.8; DB 1; Length 25;
Best Local Similarity 86.7%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      8 TACGGGTACAGGAG 22
Db      17 TCCTGTACAGGAG 3

RESULT 68
US-09-555-362-122
; Sequence 122, Application US/09555362
; GENERAL INFORMATION:
; APPLICANT: Bradfield, Christopher A.
; APPLICANT: Gu, Yi Zhong
; APPLICANT: Hogenesch, John B.
; TITLE OF INVENTION: cDNAs and Proteins Involved in Hypoxia, Circadian and Orphan Sign
; FILE REFERENCE: WARF-0044 (P98022)
; CURRENT APPLICATION NUMBER: US/09/555,362
; CURRENT FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: PCT/US98/25314
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/066,863
; PRIOR FILING DATE: 1997-11-28
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 122
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-555-362-122

Query Match      40.7%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 48;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 GCCTACGGTAC 16
Db      1 GCCTACGGTTC 13

RESULT 69
US-10-287-787-6950/c
; Sequence 6950, Application US/10287787
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Caulobacter crescentus complete genome.
; FILE REFERENCE: Jim Zeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,787
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 27958
; SOFTWARE: Proprietary
; SEQ ID NO 6950
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Caulobacter crescentus complete genome.
; FEATURE:
; LOCATION: (946131)...(946146)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 76;
US-10-287-787-6950

Query Match      40.7%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 56;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGGAGTCCAGG 28
Db      14 CAGGGCGTCCAGG 2

RESULT 70
US-10-287-787-20271/c
; Sequence 20271, Application US/10287787
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Caulobacter crescentus complete genome.
; FILE REFERENCE: Jim Zeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,787
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 27958
; SOFTWARE: Proprietary
; SEQ ID NO 20271
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Caulobacter crescentus complete genome.
; FEATURE:
; LOCATION: (303568)...(3035702)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 2244
US-10-287-787-20271

Query Match      40.7%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 56;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGGAGTCCAGG 28
Db      14 CAGGGCGTCCAGG 2

RESULT 71
US-09-590-522-1
; Sequence 1, Application US/09590522
; GENERAL INFORMATION:
; APPLICANT: Dale, Roderic M.K.
; APPLICANT: Arrow, Amy
; APPLICANT: Thompson, Terry
; TITLE OF INVENTION: Homeopathic Anti-Inflammatory
; FILE REFERENCE: OLIG-023
; CURRENT APPLICATION NUMBER: US/09/590,522
; CURRENT FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 1
; LENGTH: 16
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-590-522-1

Query Match
Best Local Similarity 40.7%; Score 11.4; DB 1; Length 16;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CCGTACAGGGAG 22
      ||||| |||||
Db 1 CCGTCCAGGAG 13

RESULT 72
PCT-US02-25943-46322/c
; Sequence 46322, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 46322
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (4497630)...(4497646)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 49628
PCT-US02-25943-46322

Query Match
Best Local Similarity 40.7%; Score 11.4; DB 1; Length 17;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGAGTCCAG 27
      ||||| |||||
Db 13 ACAGGGTGTCCAG 1

RESULT 73
PCT-US02-25943-46323/c
; Sequence 46323, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 46323
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (4497630)...(4497646)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 49628
PCT-US02-25943-46323

Query Match
Best Local Similarity 40.7%; Score 11.4; DB 1; Length 17;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGAGTCCAG 27
      ||||| |||||
Db 13 ACAGGGTGTCCAG 1
```

```
RESULT 74
US-09-745-237A-643/c
; Sequence 643, Application US/09745237A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 643
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-643

Query Match
Best Local Similarity 40.7%; Score 11.4; DB 1; Length 17;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GTGTACAGGGAGT 23
      ||||| |||||
Db 15 GTGTACAGCGAGT 3

RESULT 75
US-09-745-237A-1045/c
; Sequence 1045, Application US/09745237A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1045
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-1045

Query Match
Best Local Similarity 40.7%; Score 11.4; DB 1; Length 17;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GTGTACAGGGAGT 23
      ||||| |||||
Db 17 GTGTACAGCGAGT 5

RESULT 76
US-09-745-237A-1120/c
; Sequence 1120, Application US/09745237A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1120
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
```

US-09-745-237A-1120

Query Match 40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 76;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GTGTACAGCGAGT 23
| | | | | | | | | |
Db 14 GTGTACAGCGAGT 2

RESULT 77

US-09-930-423-643/c

; Sequence 643, Application US/09930423
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBH00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 643
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-643

Query Match 40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 76;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GTGTACAGCGAGT 23
| | | | | | | | | |
Db 15 GTGTACAGCGAGT 3

RESULT 78

US-09-930-423-1045/c

; Sequence 1045, Application US/09930423
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBH00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1045
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1045

Query Match 40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 76;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GTGTACAGCGAGT 23
| | | | | | | | | |
Db 17 GTGTACAGCGAGT 5

RESULT 79

US-09-930-423-1120/c

; Sequence 1120, Application US/09930423
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry

; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBH00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1120
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1120

Query Match 40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 76;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GTGTACAGCGAGT 23
| | | | | | | | | |
Db 14 GTGTACAGCGAGT 2

RESULT 80

US-10-227-565-46322/c

; Sequence 46322, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 46322
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; LOCATION: (4497630) ... (4497646)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 496;
US-10-227-565-46322

Query Match 40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 76;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGAGTCCAG 27
| | | | | | | | | |
Db 13 ACAGGAGTCCAG 1

RESULT 81

US-10-227-565-46323/c

; Sequence 46323, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 46323
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; LOCATION: (4497630) ... (4497646)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 496;
US-10-227-565-46323

Query Match 40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 76;

```
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGGAGTCCAG 27
Db 13 ACAGGGTGTCCAG 1

RESULT 82
US-10-310-188-68063
; Sequence 68063, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 68063
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-68063

Query Match 40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 76;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 CAGGGAGTCCAG 28
Db 1 CAGGGATCCAG 13

RESULT 83
US-10-310-188-77630
; Sequence 77630, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 77630
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-77630

Query Match 40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 76;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 TACAGGGAGTCCA 26
Db 5 TACAGTGTGTTCCA 17

RESULT 84
US-10-367-832A-46322/c
; Sequence 46322, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 46322
```

```
LENGTH: 17
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
FEATURE:
; LOCATION: (4497630)...(4497646)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 4962
US-10-367-832A-46322

Query Match 40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 76;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGGAGTCCAG 27
Db 13 ACAGGGTGTCCAG 1

RESULT 85
US-10-367-832A-46323/c
; Sequence 46323, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 46323
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (4497630)...(4497646)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 496;
US-10-367-832A-46323

Query Match 40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 76;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGGAGTCCAG 27
Db 13 ACAGGGTGTCCAG 1

RESULT 86
PCT-US02-40948-342/c
; Sequence 342, Application PC/TUS0240948
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: JONES, Karen Anne
; APPLICANT: VALDES, Ana
; APPLICANT: TOWNLEY, David J.
; APPLICANT: MANGION, Johnathan M.
; APPLICANT: GALWEY, Nicolas
; APPLICANT: BENNETT, Simon T.
; APPLICANT: MCKAY, Ian J.
; APPLICANT: SCHAFER, Alan
; TITLE OF INVENTION: NUCLEOTIDE POLYMORPHISMS ASSOCIATED WITH OSTEOPOROSIS
; FILE REFERENCE: PV-0015 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/40948
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,711
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/423,559
; PRIOR FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 400
; SOFTWARE: PERL Program
; SEQ ID NO 342
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
```

FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: NOT304 B Primer Sequence
PCT-US02-40948-342

Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 71;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 11 GTGTACAGGAGTCCA 26
DB 16 GAGTCCAGCGAGTCCA 1

RESULT 87
PCT-US95-03316-23
Sequence 23, Application PC/TUS9503316
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS GENE, SOMATIC MUTATIONS IN THE MTS
TITLE OF INVENTION: GENE, AND METHODS FOR DIAGNOSIS, PROGNOSIS AND THERAPY OF
TITLE OF INVENTION: CANCER DUE TO THE MTS GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,088
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,581
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 24884-109348-PCT-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4848
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PCT-US95-03316-23

Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 71;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGTGTACAGGAGTCC 25
DB 1 CGTGTCCAGGAGGCC 16

RESULT 88
PCT-US95-03537-23
Sequence 23, Application PC/TUS9503537
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND
TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS
TITLE OF INVENTION: GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03537
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 24884-109348-PCT-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4848
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PCT-US95-03537-23

Query Match 40.0%; Score 11.2; DB 1; Length 16;

Best Local Similarity 81.2%; Pred. No. 71;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTACAGGAGTCC 25
|||||
DB 1 CGGTCCAGGAGCCC 16

RESULT 89

US-08-474-083-23
; Sequence 23, Application US/08474083
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Cannon-Albright, Lisa A.
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: GEMLINE MUTATIONS IN THE MTS GENE AND
; TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS
; TITLE OF INVENTION: GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,083
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03537
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; NAME: Imnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-G
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-474-083-23

Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 71;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTACAGGAGTCC 25
|||||
DB 1 CGGTCCAGGAGCCC 16

RESULT 90

US-08-479-731-23
; Sequence 23, Application US/08479731
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,731
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Imnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-479-731-23

Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 71;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTACAGGAGTCC 25
Db 1 CGGTCCAGGAGCCC 16

RESULT 91
US-08-481-063-23
; Sequence 23, Application US/08481063
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: SOMATIC MUTATIONS IN THE MTS GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,063
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-481-063-23

Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 71;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTACAGGAGTCC 25
Db 1 CGGTCCAGGAGCCC 16

RESULT 92
US-10-310-188-34900
; Sequence 34900, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 34900
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-310-188-34900

Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 71;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 13 GTACAGGAGTCCAGG 28
Db 1 GTGAGGTAGTCCAGG 16

RESULT 93
PCT-US02-16840-1766
; Sequence 1766, Application PC/TUS0216840
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Leve
; FILE REFERENCE: 400/046 (MBHB02-326)
; CURRENT APPLICATION NUMBER: PCT/US02/16840
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/294,140
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 6810
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1766
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; PCT-US02-16840-1766

Query Match 40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGGAG 22
Db 1 CCACCAGUACAGGAG 16

RESULT 94
PCT-US02-16840A-1766
; Sequence 1766, Application PC/TUS0216840A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Leve
; TITLE OF INVENTION: RAS, HER2 and HIV
; FILE REFERENCE: 400/046 (MBHB02-326)

; CURRENT APPLICATION NUMBER: PCT/US02/16840A
 ; CURRENT FILING DATE: 2002-05-29
 ; PRIOR APPLICATION NUMBER: US 60/318,471
 ; PRIOR FILING DATE: 2001-09-10
 ; PRIOR APPLICATION NUMBER: US 60/296,249
 ; PRIOR FILING DATE: 2001-06-06
 ; PRIOR APPLICATION NUMBER: US 60/294,140
 ; PRIOR FILING DATE: 2001-05-29
 ; NUMBER OF SEQ ID NOS: 6810
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 1766
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 ; PCT-US02-16840A-1766

Query Match 40.0%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 75.0%; Pred. No. 82;
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 CTACGTGTACAGGAG 22
 Db 1 CCACCAGUACAGGAG 16

RESULT 95
 US-09-546-745A-6677
 ; Sequence 6677, Application US/09546745A
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Blatt, Larry
 ; APPLICANT: Zwick, Michael
 ; APPLICANT: Pavco, Pam
 ; APPLICANT: McSwiggen, Jim
 ; TITLE OF INVENTION: Regulation of Repressor Genes using Nucleic Acid Molecules
 ; FILE REFERENCE: 237/193
 ; CURRENT APPLICATION NUMBER: US/09/546,745A
 ; CURRENT FILING DATE: 2000-04-11
 ; NUMBER OF SEQ ID NOS: 7043
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 6677
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
 ; US-09-546-745A-6677

Query Match 40.0%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 62.5%; Pred. No. 82;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 7 CTACGTGTACAGGAG 22
 Db 1 CUACAUGUACAGGAG 16

RESULT 96
 US-09-818-875-2950/c
 ; Sequence 2950, Application US/09818875
 ; GENERAL INFORMATION:
 ; APPLICANT: Knies, Eric B.
 ; APPLICANT: Gamber, Howard B.
 ; APPLICANT: Rice, Michael C.
 ; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
 ; FILE REFERENCE: Napro-4
 ; CURRENT APPLICATION NUMBER: US/09/818,875
 ; CURRENT FILING DATE: 2001-03-27
 ; PRIOR APPLICATION NUMBER: US 60/192,176
 ; PRIOR FILING DATE: 2000-03-27
 ; PRIOR APPLICATION NUMBER: US 60/192,179
 ; PRIOR FILING DATE: 2000-03-27

; PRIOR APPLICATION NUMBER: US 60/208,538
 ; PRIOR FILING DATE: 2000-06-01
 ; PRIOR APPLICATION NUMBER: US 60/244,989
 ; PRIOR FILING DATE: 2000-10-30
 ; NUMBER OF SEQ ID NOS: 4385
 ; SOFTWARE: Friedman macro Napro-4
 ; SEQ ID NO 2950
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-818-875-2950

Query Match 40.0%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 82;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 ACGTGTACAGGAGTC 24
 Db 17 ACTGTCCAGGGAGGC 2

RESULT 97
 US-09-818-875-2951
 ; Sequence 2951, Application US/09818875
 ; GENERAL INFORMATION:
 ; APPLICANT: Knies, Eric B.
 ; APPLICANT: Gamber, Howard B.
 ; APPLICANT: Rice, Michael C.
 ; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
 ; FILE REFERENCE: Napro-4
 ; CURRENT APPLICATION NUMBER: US/09/818,875
 ; CURRENT FILING DATE: 2001-03-27
 ; PRIOR APPLICATION NUMBER: US 60/192,176
 ; PRIOR FILING DATE: 2000-03-27
 ; PRIOR APPLICATION NUMBER: US 60/192,179
 ; PRIOR FILING DATE: 2000-03-27
 ; PRIOR APPLICATION NUMBER: US 60/208,538
 ; PRIOR FILING DATE: 2000-06-01
 ; PRIOR APPLICATION NUMBER: US 60/244,989
 ; PRIOR FILING DATE: 2000-10-30
 ; NUMBER OF SEQ ID NOS: 4385
 ; SOFTWARE: Friedman macro Napro-4
 ; SEQ ID NO 2951
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-818-875-2951

Query Match 40.0%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 82;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 ACGTGTACAGGAGTC 24
 Db 1 ACTGTCCAGGGAGGC 16

RESULT 98
 US-09-922-181A-1343
 ; Sequence 1343, Application US/09922181A
 ; GENERAL INFORMATION:
 ; APPLICANT: Gu, Yizhong
 ; APPLICANT: Shannan, Mark
 ; APPLICANT: Nguyen, Cung-Tuong
 ; TITLE OF INVENTION: FOUR HUMAN ZINC-FINGER-CONTAINING PROTEINS: MD23, MD24, MD27 AND
 ; FILE REFERENCE: AEOMICA-12
 ; CURRENT APPLICATION NUMBER: US/09/922,181A
 ; CURRENT FILING DATE: 2001-12-12
 ; NUMBER OF SEQ ID NOS: 7046
 ; SOFTWARE: Aecomica Sequence Listing Engine
 ; SEQ ID NO 1343
 ; LENGTH: 17


```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-181A-1343

Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTGACAGGAGTCC 25
Db 1 CGGTGACAGGAGTGC 16

RESULT 99
US-10-156-306-7026
; Sequence 7026, Application US/10156306
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156.306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7026
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-7026

Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 82;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 12 TGTACAGGAGTCCAG 27
Db 2 UGCAGAGGAGUACAG 17

RESULT 100
US-10-156-306-7027
; Sequence 7027, Application US/10156306
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156.306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7027
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-7027

Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 82;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 12 TGTACAGGAGTCCAG 27
Db 1 UGCAGAGGAGUACAG 16

RESULT 101
US-10-209-787-2950/c
; Sequence 2950, Application US/10209787
; GENERAL INFORMATION:
; APPLICANT: Knies, Eric B.
; APPLICANT: Gamber, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/10/209,787
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2951
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-209-787-2951

Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ACGTGACAGGAGTGC 24
Db 1 ACTTGCCAGGAGGC 16

RESULT 102
US-10-209-787-2951
; Sequence 2951, Application US/10209787
; GENERAL INFORMATION:
; APPLICANT: Knies, Eric B.
; APPLICANT: Gamber, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/10/209,787
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2951
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-209-787-2951

Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ACGTGACAGGAGTGC 24
Db 1 ACTTGCCAGGAGGC 16
```

```
RESULT 103
US-10-238-700-3087
; Sequence 2951, Application US/10261185
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4CON
; CURRENT APPLICATION NUMBER: US/10/261,185
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/09761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2951
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-238-700-3087

Query Match          40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGGAG 22
DB 1 CCACCAGUACAGGAG 16

RESULT 104
US-10-261-185-2950/c
; Sequence 2950, Application US/10261185
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4CON
; CURRENT APPLICATION NUMBER: US/10/261,185
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/09761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2950
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-261-185-2950

Query Match          40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 ACGTGTACGGGAGTC 24
DB 17 ACTGTCCAGGAGGC 2

RESULT 105
US-10-261-185-2951
; Sequence 2951, Application US/10261185
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4CON
; CURRENT APPLICATION NUMBER: US/10/261,185
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/09761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2951
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-261-185-2951

Query Match          40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 ACGTGTACGGGAGTC 24
DB 1 ACTGTCCAGGAGGC 16

RESULT 106
US-10-310-188-41474
; Sequence 41474, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41474
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-41474

Query Match          40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCGCTACGTGTACAGG 19
DB 2 GCGCTACGATTACAGG 17

RESULT 107
US-10-310-188-74621/c
; Sequence 74621, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
```



```
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-623-107-2950

Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 ACGTGACAGGGAGTC 24
   |||||
Db 17 ACTTGCCAGGGAGGC 2

RESULT 112
US-10-623-107-2951
; Sequence 2951, Application US/10623107
; GENERAL INFORMATION:
; APPLICANT: KMEC, ERIC B.
; TITLE OF INVENTION: TARGETED NUCLEIC ACID SEQUENCE ALTERATION USING PLURAL
; FILE REFERENCE: OLIGONUCLEOTIDES
; CURRENT APPLICATION NUMBER: US/10/623,107
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/397,555
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 7046
; SOFTWARE: PatentIn ver 3.2
; SEQ ID NO 2951
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-623-107-2951

Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 ACGTGACAGGGAGTC 24
   |||||
Db 17 ACTTGCCAGGGAGGC 16

RESULT 113
US-10-681-074-2950/c
; Sequence 2950, Application US/10681074
; GENERAL INFORMATION:
; APPLICANT: KMEC, ERIC B.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REDUCING SCREENING IN
; FILE REFERENCE: OLIGONUCLEOTIDE-DIRECTED NUCLEIC ACID SEQUENCE ALTERATION
; CURRENT APPLICATION NUMBER: US/10/681,074
; PRIOR FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: US 60/453,360
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US 60/416,983
; NUMBER OF SEQ ID NOS: 4375
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2950
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-681-074-2950

Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 ACGTGACAGGGAGTC 24
   |||||
Db 17 ACTTGCCAGGGAGGC 2
```

```
RESULT 114
US-10-681-074-2951
; Sequence 2951, Application US/10681074
; GENERAL INFORMATION:
; APPLICANT: KMEC, ERIC B.
; APPLICANT: VAN BRABANT, ANJA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REDUCING SCREENING IN
; FILE REFERENCE: OLIGONUCLEOTIDE-DIRECTED NUCLEIC ACID SEQUENCE ALTERATION
; CURRENT APPLICATION NUMBER: US/10/681,074
; PRIOR FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: US 60/453,360
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US 60/416,983
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 4375
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2951
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-681-074-2951
```

```
Query Match      40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 9 ACGTGACAGGGAGTC 24
   |||||
Db 1 ACTTGCCAGGGAGGC 16
```

```
RESULT 115
US-10-724-270-1766
; Sequence 1766, Application US/10724270
; GENERAL INFORMATION:
; APPLICANT: MCSwigen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Leve
; FILE REFERENCE: 400/046-US (MBH02-326-A)
; CURRENT APPLICATION NUMBER: US/10/724,270
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: PCT/US02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/294,140
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 10/238,700
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 10/157,580
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 6810
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1766
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-724-270-1766
```

```
Query Match          40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      7 CTACGTGTACAGGGAG 22
        |||:|||||
Db       1 CCACCAGUACAGGGAG 16
        |||:|||||

RESULT 116
US-60-339-764-2158/c
; Sequence 2158, Application US/60339764
; GENERAL INFORMATION:
; APPLICANT: Guo, Jinjiao
; TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1
; FILE REFERENCE: AEWICA-31
; CURRENT APPLICATION NUMBER: US/60/339,764
; NUMBER OF SEQ ID NOS: 3310
; SOFTWARE: Aewica Sequence Listing Engine
; SEQ ID NO 2158
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-339-764-2158

Query Match          40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      13 GTACAGGAGTCCAGG 28
        |||:|||||
Db       17 GAAAGGAGTCAAGG 2
        |||:|||||

RESULT 117
US-60-339-764-2160/c
; Sequence 2160, Application US/60339764
; GENERAL INFORMATION:
; APPLICANT: Guo, Jinjiao
; TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1
; FILE REFERENCE: AEWICA-31
; CURRENT APPLICATION NUMBER: US/60/339,764
; NUMBER OF SEQ ID NOS: 3310
; SOFTWARE: Aewica Sequence Listing Engine
; SEQ ID NO 2160
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-339-764-2160

Query Match          40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      12 TGTACAGGAGTCCAG 27
        |||:|||||
Db       16 TGAAGAGGAGTCAAG 1
        |||:|||||

RESULT 118
US-60-339-764-2303/c
; Sequence 2303, Application US/60339764
; GENERAL INFORMATION:
; APPLICANT: Guo, Jinjiao
; TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1
; FILE REFERENCE: AEWICA-31
; CURRENT APPLICATION NUMBER: US/60/339,764
; NUMBER OF SEQ ID NOS: 3310
; SOFTWARE: Aewica Sequence Listing Engine
; SEQ ID NO 2303
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-339-764-2303

Query Match          40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 82;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5 CCTACGTGTACAGGG 20
        |||:|||||
Db       16 CCTACGTATTAAGAG 1
        |||:|||||

RESULT 120
US-10-305-275-941/c
; Sequence 941, Application US/10305275
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Aeropyrum pernix K1 complete genome.
; FILE REFERENCE: Jim Zeiger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/305,275
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Proprietary
; SEQ ID NO 941
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Aeropyrum pernix K1 complete genome.
; FEATURE:
; LOCATION: (845005)...(845019)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectionObjectNumber = 13;
US-10-305-275-941

Query Match          39.3%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      18 GGGAGTCCAGG 28
        |||:|||||
Db       15 GGGAGTCCAGG 5
        |||:|||||

RESULT 121
US-10-305-275-942/c
; Sequence 942, Application US/10305275
```

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; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Aeropyrum pernix K1 complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/305,275
; CURRENT FILING DATE: 2002-11-28
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: Proprietary
; SEQ ID NO 942
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Aeropyrum pernix K1 complete genome.
; FEATURE:
; LOCATION: (845005)...(845019)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 1328
US-10-305-275A-942

Query Match      39.3%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      18 GGGAGTCCAGG 28
      |||||
Db      15 GGGAGTCCAGG 5

RESULT 124
US-10-310-188-56454
; Sequence 56454, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 56454
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-56454

Query Match      39.3%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 TGTACAGGGAG 22
      |||||
Db      6 TGTACAGGGAG 16

RESULT 125
PCT-US01-44838-5/c
; Sequence 5, Application PC/TUS0144838
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; TITLE OF INVENTION: Genetic Typing of Human Genes And Related Materials And Methods
; FILE REFERENCE: 4389-23-PCT
; CURRENT APPLICATION NUMBER: PCT/US01/44838
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 1449
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-44838-5

Query Match      38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 71;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      15 ACAGGGAGTCCAGG 28
      |||||
Db      15 ACAGGGTTCCAGG 2

RESULT 126
PCT-US02-25943-41393/c
; Sequence 41393, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943

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;; CURRENT FILING DATE: 2002-08-27
;; NUMBER OF SEQ ID NOS: 64158
;; SOFTWARE: Proprietary
;; SEQ ID NO 41393
;; LENGTH: 15
;; TYPE: DNA
;; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
;; FEATURE:
;; LOCATION: (4017819)...(4017834)
;; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 44331
FCT-US62-25943-41393

Query Match 38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 71;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 GTACAGGAGTGCA 26
Db 15 GCACAGGTAGTGCA 2

RESULT 127
US-08-774-306-121
; Sequence 121, Application US/08774306
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,306
; FILING DATE: 26-DEC-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/182,968
; FILING DATE: 13-JANUARY-1994
; APPLICATION NUMBER: 07/882,888
; FILING DATE: 14-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 953-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-774-306-121
Query Match 38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 71;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCCCTACGTGTA 15
Db 1 GGGCCCCCGUGCA 14

RESULT 128
US-09-274-553-678
; Sequence 678 Application US/09274553A
; GENERAL INFORMATION:
; APPLICANT: RIBOZYNE PHARMACEUTICALS, INC.
; APPLICANT: 2950 Wilderness Place
; APPLICANT: Boulder, Colorado 80301
; APPLICANT: USA
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS RELATED TO HEPATITIS C
; TITLE OF INVENTION: VIRUS INFECTION
; FILE REFERENCE: 241/078-FCT
; CURRENT APPLICATION NUMBER: US/09/274,553A
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3118
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 678
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Hepatitis C Virus
US-09-274-553-678

Query Match 38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 71;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCCCTACGTGTA 15
Db 1 GGGCCCCCGUGCA 14

RESULT 129
US-09-274-553B-143
; Sequence 143, Application US/09274553B
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: IPI 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553B
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 143
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553B-143

```
;
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-143

Query Match      38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 71;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCCCTACGTGTA 15
   |||||: ||: ||
Db 1 GGGCCCUCCGUGCA 14

RESULT 130
US-09-274-553C-143
; Sequence 143, Application US/09274553C
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: tpi 247/282
; CURRENT APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-02-24
; PRIOR FILING DATE: 1998-09-18
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 143
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553C-143

Query Match      38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 71;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCCCTACGTGTA 15
   |||||: ||: ||
Db 1 GGGCCCUCCGUGCA 14

RESULT 131
US-09-274-553D-143
; Sequence 143, Application US/09274553D
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: tpi 247/282
; CURRENT APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-02-24
; PRIOR FILING DATE: 1998-09-18
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 143
; LENGTH: 15
```

```
;
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-143

Query Match      38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 71;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCCCTACGTGTA 15
   |||||: ||: ||
Db 1 GGGCCCUCCGUGCA 14

RESULT 132
US-09-274-553E-143
; Sequence 143, Application US/09274553E
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT
; FILE REFERENCE: tpi 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553E
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 143
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553E-143

Query Match      38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 71;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCCCTACGTGTA 15
   |||||: ||: ||
Db 1 GGGCCCUCCGUGCA 14

RESULT 133
US-09-504-231A-143
; Sequence 143, Application US/09504231A
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT
; FILE REFERENCE: tpi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
```



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; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 143
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-143

Query Match      38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 71;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 GGGCCCTACGTGTA 15
        |||||: |||:|
Db      1 GGGCCCUCCGUGCA 14

RESULT 134
US-09-504-231B-143
; Sequence 143, Application US/09504231B
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: M8H00-801-A (247/282)
; CURRENT APPLICATION NUMBER: US/09/504,231B
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; NUMBER OF SEQ ID NOS: 3258
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 143
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231B-143

Query Match      38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 71;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 GGGCCCTACGTGTA 15
        |||||: |||:|
Db      1 GGGCCCUCCGUGCA 14

RESULT 135
US-09-611-931-143
; Sequence 143, Application US/09611931
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: M8H00-801-B (250/285)
; CURRENT APPLICATION NUMBER: US/09/611,931A
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 143
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Hepatitis C Virus
US-09-611-931A-143

Query Match      38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 71;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 GGGCCCTACGTGTA 15
        |||||: |||:|
Db      1 GGGCCCUCCGUGCA 14

RESULT 137
US-09-633-515-121
; Sequence 121, Application US/09633515
```

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; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: Ipi 250/285
; CURRENT APPLICATION NUMBER: US/09/611,931
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 143
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-611-931-143

Query Match      38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 71;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 GGGCCCTACGTGTA 15
        |||||: |||:|
Db      1 GGGCCCUCCGUGCA 14

RESULT 136
US-09-611-931A-143
; Sequence 143, Application US/09611931A
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: M8H00-801-B (250/285)
; CURRENT APPLICATION NUMBER: US/09/611,931A
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 143
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Hepatitis C Virus
US-09-611-931A-143

Query Match      38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 71;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 GGGCCCTACGTGTA 15
        |||||: |||:|
Db      1 GGGCCCUCCGUGCA 14

RESULT 137
US-09-633-515-121
; Sequence 121, Application US/09633515
```

GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR
INHIBITING HEPATITIS C
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 498
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: California
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/633,515
FILING DATE: 2000-08-07

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/064,156
FILING DATE: April 21, 1998
APPLICATION NUMBER: 08/182,968
FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/882,888
FILING DATE: May 14, 1992

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 234/083
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-633-515-121

Query Match 38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 71;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCCCTACGTGTA 15
DB 1 GGGCCCTACGTGTA 14

RESULT 138
US-09-724-389-5/c
Sequence 5, Application US/09724389
GENERAL INFORMATION:
APPLICANT: Guida, Marco
APPLICANT: Hall, Jeff
TITLE OF INVENTION: Genetic Typing of Human Genes and Related Materials and Methods
CURRENT APPLICATION NUMBER: US/09/724,389
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 1449
SOFTWARE: Patent in version 3.0
SEQ ID NO 5
LENGTH: 15
TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-389-5

Query Match 38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 71;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 15 ACAGGGAGTCCAGG 28
DB 15 ACAGGGAGTCCAGG 2

RESULT 139
US-10-227-565-41393/c
Sequence 41393, Application US/10227565
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/227,565
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 64158
SOFTWARE: Proprietary
SEQ ID NO 41393
LENGTH: 15
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
FEATURE:
LOCATION: (4017819)...(4017834)
OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 443;
US-10-227-565-41393

Query Match 38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 71;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 GTACAGGAGTCCCA 26
DB 15 GCACAGGTAGTCCA 2

RESULT 140
US-10-367-832A-41393/c
Sequence 41393, Application US/10367832A
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/367,832A
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 64158
SOFTWARE: Proprietary
SEQ ID NO 41393
LENGTH: 15
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
FEATURE:
LOCATION: (4017819)...(4017834)
OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 443;
US-10-367-832A-41393

Query Match 38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 71;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 GTACAGGAGTCCCA 26
DB 15 GCACAGGTAGTCCA 2

RESULT 141
US-10-310-188-34441
Sequence 34441, Application US/10310188
GENERAL INFORMATION:
APPLICANT: Rosettacemomics
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEI

; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34441
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-34441

Query Match 38.6%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 82;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 ACAGGAGTCCAGG 28
|||||
Db 3 ACAGGAGTCCAGG 16

RESULT 142
PCT-US03-10296-20/c
; Sequence 20, Application PC/TUS0310296
; GENERAL INFORMATION:
; APPLICANT: New England Biolabs, Inc.
; TITLE OF INVENTION: Methods And Compositions For DNA Manipulation
; FILE REFERENCE: NEB-203-US
; CURRENT APPLICATION NUMBER: PCT/US03/10296
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/372,352
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 60/372,675
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/421,010
; PRIOR FILING DATE: 2002-10-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 12
; TYPE: DNA
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: mutated pUC19
PCT-US03-10296-20

Query Match 37.1%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 47;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCTACGTGTACAG 17
|||||
Db 12 CCTAGGTGTACA 1

RESULT 143
US-10-407-637-20/c
; Sequence 20, Application US/10407637
; GENERAL INFORMATION:
; APPLICANT: Bitinaite, Jurate
; TITLE OF INVENTION: Methods And Compositions For DNA Manipulation
; FILE REFERENCE: NEB-203-US
; CURRENT APPLICATION NUMBER: US/10/407,637
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/372,352
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US 60/372,675
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/421,010
; PRIOR FILING DATE: 2002-10-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20

; LENGTH: 12
; TYPE: DNA
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: mutated pUC19
US-10-407-637-20

Query Match 37.1%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 47;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCTACGTGTACA 17
|||||
Db 12 CCTAGGTGTACA 1

RESULT 144
PCT-US01-18815-7
; Sequence 7, Application PC/TUS0118815
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Anastasio, Alison E.
; APPLICANT: Duda, Amy
; APPLICANT: Kliehm, Stefanie E.
; APPLICANT: Koshy, Beena
; APPLICANT: Sausker, Elizabeth Ann
; TITLE OF INVENTION: Haplotypes of the CFL1 Gene
; FILE REFERENCE: MMH-0706PCT CFL1
; CURRENT APPLICATION NUMBER: PCT/US01/18815
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/210,894
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-18815-7

Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 82;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCCTACGTGTACAG 18
|||||
Db 2 CCCTACRTGCACGTG 15

RESULT 145
PCT-US01-26215-16
; Sequence 16, Application PC/TUS0126215
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bieglecki, Karyn M
; APPLICANT: Chew, Anne
; APPLICANT: Duda, Amy
; APPLICANT: Finkel, Kevin
; APPLICANT: Han, Jin-Rua
; APPLICANT: Messer, Chad
; APPLICANT: Tirrell, Charles
; TITLE OF INVENTION: HAPLOTYPES OF THE ADH4 GENE
; FILE REFERENCE: ADH4 MMH1088-PCT
; CURRENT APPLICATION NUMBER: PCT/US01/26215
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,816
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens

```
PCT-US01-26215-16
Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 82;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 14 TACAGGAGTCCAG 27
Db 2 TAAAGGAGACCAG 15

RESULT 146
PCT-US01-26488-60
; Sequence 60, Application PC/TUS0126488
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Anastasio, Alison E
; APPLICANT: Chew, Anne
; APPLICANT: Choi, Julie Y
; APPLICANT: Kazemi, Amir
; APPLICANT: Kliem, Stefanie E
; APPLICANT: Koshiy, Beena
; APPLICANT: Kumar, Anant Madan
; APPLICANT: Parks, Katie E
; TITLE OF INVENTION: HAPLOTYPES OF THE MTHFR GENE
; FILE REFERENCE: MTHFR MHL077-PC1
; CURRENT APPLICATION NUMBER: PCT/US01/26488
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227,757
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 60
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-26488-60

Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 82;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGAC 16
Db 2 GTCCCAACGTGTC 15

RESULT 147
PCT-US01-47434-7/c
; Sequence 7, Application PC/TUS0147434
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Sausher, Elizabeth Ann
; APPLICANT: Shah, Nisha
; TITLE OF INVENTION: HAPLOTYPES OF THE GPR6 GENE
; FILE REFERENCE: GPR6 MMH-1648PCT
; CURRENT APPLICATION NUMBER: PCT/US01/47434
; CURRENT FILING DATE: 2001-10-22
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo Sapiens
PCT-US01-47434-7

Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

PCT-US01-26215-16
Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 17 AGGAGTCCAG 28
Db 12 AGGAGTCCAG 1

RESULT 148
PCT-US02-25940-18950/c
; Sequence 18950, Application PC/TUS0225940
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25940
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 18950
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (2303965)...(2303980)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 2219
PCT-US02-25940-18950

Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 CAGGAGTCCAG 27
Db 13 CAGGAGTCCAG 2

RESULT 149
PCT-US02-25942-4864/c
; Sequence 4864, Application PC/TUS0225942
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid ps
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25942
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 15792
; SOFTWARE: Proprietary
; SEQ ID NO 4864
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps
; FEATURE:
; LOCATION: (1267742)...(1267757)
; OTHER INFORMATION: Chromosome = 2 Strand = positive ConnectronObjectNumber = 501
PCT-US02-25942-4864

Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 CAGGAGTCCAG 27
Db 15 CAGGAGTCCAG 4

RESULT 150
PCT-US02-25942-6581/c
; Sequence 6581, Application PC/TUS0225942
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid ps
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25942
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 15792
```

```
; SOFTWARE: Proprietary
; SEQ ID NO 6581
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps
; FEATURE:
; LOCATION: (3538785)...(3538798)
; OTHER INFORMATION: Chromosome = 3 Strand = negative ConnectronObjectNumber = 20087
PCT-US02-25942-6581

Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CAGGAGTCCAG 27
    |||||
DB 15 CAGGAAGTCCAG 4

RESULT 151
PCT-US02-25943-22682/c
; Sequence 22682, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 22682
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (2239343)...(2239357)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 24384
PCT-US02-25943-22682

Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CAGGAGTCCAG 27
    |||||
DB 15 CAGGTAGTCCAG 4

RESULT 152
PCT-US02-25943-34828/c
; Sequence 34828, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 34828
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3391804)...(3391817)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 37318
PCT-US02-25943-34828

Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CAGGAGTCCAG 27
```

```
|||||
DB 15 CAGGTAGTCCAG 4

RESULT 153
PCT-US02-25943-37161/c
; Sequence 37161, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 37161
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3645015)...(3645029)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 3983
PCT-US02-25943-37161

Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 CAGGAGTCCAG 27
    |||||
DB 15 CAGGTAGTCCAG 4

RESULT 154
PCT-US02-25943-48484
; Sequence 48484, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 48484
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (4677818)...(4677832)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 5192
PCT-US02-25943-48484

Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 CAGGAGTCCAG 27
    |||||
DB 3 CAGGAGTCCAG 14

RESULT 155
PCT-US02-25943-62741
; Sequence 62741, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
```

```
; SEQ ID NO 62741
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (6120631)...(6120645)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 67218
PCT-US02-25943-62741

Query Match          37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGAGTCCAG 27
      ||||| |||||
Db       3 CAGGAGTCCAG 14

RESULT 156
US-10-227-563-18950/c
; Sequence 18950, Application US/10227563
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zeiger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,563
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 18950
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (2303965)...(2303980)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 22195
US-10-227-563-18950

Query Match          37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGAGTCCAG 27
      ||||| |||||
Db       13 CAGGAGTCCAG 2

RESULT 157
US-10-227-565-22682/c
; Sequence 22682, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeiger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 22682
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (2239343)...(2239357)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 24384
US-10-227-565-22682

Query Match          37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGAGTCCAG 27
      ||||| |||||
Db       15 CAGGAGTCCAG 4

RESULT 158
US-10-227-565-34828/c
; Sequence 34828, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeiger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 34828
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3391804)...(3391817)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 3731
US-10-227-565-34828

Query Match          37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGAGTCCAG 27
      ||||| |||||
Db       15 CAGGAGTCCAG 4

RESULT 159
US-10-227-565-37161/c
; Sequence 37161, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeiger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 37161
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3645015)...(3645029)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 3983
US-10-227-565-37161

Query Match          37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGAGTCCAG 27
      ||||| |||||
Db       15 CAGGAGTCCAG 4

RESULT 160
US-10-227-565-48484
; Sequence 48484, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeiger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 48484
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; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (4677818)...(4677832)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 51923
US-10-227-565-48484
Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 16 CAGGGAGTCCAG 27
Db 3 CAGGGACTCCAG 14
RESULT 161
US-10-227-565-62741
; Sequence 62741, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 62741
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (6120631)...(6120645)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 67218
US-10-227-565-62741
Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 16 CAGGGAGTCCAG 27
Db 3 CAGGGACTCCAG 14
RESULT 162
US-10-227-567-4864/c
; Sequence 4864, Application US/10227567
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid ps
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,567
; CURRENT FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 15792
; SOFTWARE: Proprietary
; SEQ ID NO 4864
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps
; FEATURE:
; LOCATION: (1267742)...(1267757)
; OTHER INFORMATION: Chromosome = 2 Strand = positive ConnectronObjectNumber = 5075
US-10-227-567-4864
Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 16 CAGGGAGTCCAG 27
Db 15 CAGGAAGTCCAG 4
RESULT 163
US-10-227-567-6581/c
; Sequence 6581, Application US/10227567
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid ps
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,567
; CURRENT FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 15792
; SOFTWARE: Proprietary
; SEQ ID NO 6581
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps
; FEATURE:
; LOCATION: (3538785)...(3538798)
; OTHER INFORMATION: Chromosome = 3 Strand = negative ConnectronObjectNumber = 2001
US-10-227-567-6581
Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 16 CAGGGAGTCCAG 27
Db 15 CAGGAAGTCCAG 4
RESULT 164
US-10-287-787-27958/c
; Sequence 27958, Application US/10287787
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Caulobacter crescentus complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,787
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 27958
; SOFTWARE: Proprietary
; SEQ ID NO 27958
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Caulobacter crescentus complete genome.
; FEATURE:
; LOCATION: (4016151)...(4016165)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 308
US-10-287-787-27958
Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 16 CAGGGAGTCCAG 27
Db 12 CAGGGCTCCAG 1
RESULT 165
US-10-367-729A-4864/c
; Sequence 4864, Application US/10367729A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid ps
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,729A
; CURRENT FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 15792
; SOFTWARE: Proprietary
; SEQ ID NO 4864
; LENGTH: 15
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; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps
; FEATURE:
; LOCATION: (1267742)...(1267757)
; OTHER INFORMATION: Chromosome = 2 Strand = positive ConnectronObjectNumber = 5075
US-10-367-729A-4864

Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 CAGGAGTCCAG 27
   ||| |||||
DB 15 CAGGAAGTCCAG 4

RESULT 166
US-10-367-729A-6581/c
; Sequence 6581, Application US/10367729A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Sinorhizobium meliloti complete genome, plasmid ps
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,729A
; CURRENT FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 15792
; SOFTWARE: Proprietary
; SEQ ID NO 6581
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti complete genome, plasmid ps
; FEATURE:
; LOCATION: (3538785)...(3538798)
; OTHER INFORMATION: Chromosome = 3 Strand = negative ConnectronObjectNumber = 20087
US-10-367-729A-6581

Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 CAGGAGTCCAG 27
   ||| |||||
DB 15 CAGGAAGTCCAG 4

RESULT 167
US-10-367-832A-22682/c
; Sequence 22682, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 22682
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (2239343)...(2239357)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 24384
US-10-367-832A-22682

Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 CAGGAGTCCAG 27
   ||| |||||
DB 15 CAGGAGTCCAG 4

RESULT 168
US-10-367-832A-34828/c
; Sequence 34828, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 34828
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3391804)...(3391817)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 3731
US-10-367-832A-34828

Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 CAGGAGTCCAG 27
   ||| |||||
DB 15 CAGGAGTCCAG 4

RESULT 169
US-10-367-832A-37161/c
; Sequence 37161, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 37161
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3645015)...(3645029)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 398
US-10-367-832A-37161

Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 CAGGAGTCCAG 27
   ||| |||||
DB 15 CAGGAGTCCAG 4

RESULT 170
US-10-367-832A-48484
; Sequence 48484, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 48484
; LENGTH: 15
; TYPE: DNA

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; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (4677818)...(4677832)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 51923
US-10-367-832A-48484
Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 16 CAGGGAGTCCAG 27
Db 3 CAGGGAGTCCAG 14

RESULT 171
US-10-367-832A-62741
; Sequence 62741, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 62741
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (6120631)...(6120645)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 67218
US-10-367-832A-62741
Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 16 CAGGGAGTCCAG 27
Db 3 CAGGGAGTCCAG 14

RESULT 172
US-10-367-892-18950/c
; Sequence 18950, Application US/10367892
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10367,892
; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 18950
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (2303965)...(2303980)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 22195
US-10-367-892-18950
Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 82;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 16 CAGGGAGTCCAG 27
Db 13 CAGGGAGTCCAG 2

RESULT 173
PCT-US02-25943-33165/c
; Sequence 33165, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 33165
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3237918)...(3237933)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 3554
PCT-US02-25943-33165
Query Match 37.1%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 16 CAGGGAGTCCAG 27
Db 16 CAGGTAGTCCAG 5

RESULT 174
PCT-US02-25943-33166
; Sequence 33166, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 33166
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3237919)...(3237934)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 3555
PCT-US02-25943-33166
Query Match 37.1%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 16 CAGGGAGTCCAG 27
Db 2 CAGGTAGTCCAG 13

RESULT 175
PCT-US02-25943-34829
; Sequence 34829, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 34829
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.

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; FEATURE:
; LOCATION: (3391804)...(3391818)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 37320
PCT-US02-25943-34829

Query Match      37.1%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGGAGTCCAG 27
Db      2 CAGGTAGTCCAG 13

RESULT 176
US-10-227-565-33165/c
; Sequence 33165, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 33165
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3237918)...(3237933)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 35549
US-10-227-565-33165

Query Match      37.1%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGGAGTCCAG 27
Db      16 CAGGTAGTCCAG 5

RESULT 177
US-10-227-565-33166
; Sequence 33166, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 33166
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3237919)...(3237934)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 35550
US-10-227-565-33166

Query Match      37.1%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGGAGTCCAG 27
Db      2 CAGGTAGTCCAG 13

RESULT 178
US-10-227-565-34829
; Sequence 34829, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 34829
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3391804)...(3391818)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 3732
US-10-227-565-34829

Query Match      37.1%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGGAGTCCAG 27
Db      2 CAGGTAGTCCAG 13

RESULT 179
US-10-305-274-517
; Sequence 517, Application US/10305274
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Aquifex aeolicus complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/305,274
; CURRENT FILING DATE: 2002-11-27
; NUMBER OF SEQ ID NOS: 1550
; SOFTWARE: Proprietary
; SEQ ID NO 517
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Aquifex aeolicus complete genome.
; FEATURE:
; LOCATION: (532072)...(532087)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 7;
US-10-305-274-517

Query Match      37.1%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 CGGTGTACAGGGA 21
Db      5 CGTTTACAGGGA 16

RESULT 180
US-10-305-274-1406
; Sequence 1406, Application US/10305274
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Aquifex aeolicus complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/305,274
; CURRENT FILING DATE: 2002-11-27
; NUMBER OF SEQ ID NOS: 1550
; SOFTWARE: Proprietary
; SEQ ID NO 1406
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Aquifex aeolicus complete genome.
; FEATURE:
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; LOCATION: (1394218)...(1394232)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 1909
US-10-367-832A-33165/c
Query Match 37.1%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 10 CGGTACAGGGA 21
DB 5 CGTTTACAGGGA 16
RESULT 181
US-10-367-832A-33165/c
; Sequence 33165, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 33165
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3237918)...(3237933)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 35549
US-10-367-832A-33165
Query Match 37.1%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 16 CAGGAGTCCAG 27
DB 16 CAGGTAGTCCAG 5
RESULT 182
US-10-367-832A-33166
; Sequence 33166, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,932A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 33166
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3237919)...(3237934)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 35550
US-10-367-832A-33166
Query Match 37.1%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 16 CAGGAGTCCAG 27
DB 2 CAGGTAGTCCAG 13
RESULT 183
US-10-367-832A-34829
```

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; Sequence 34829, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367,832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 34829
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3391804)...(3391818)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 373.
US-10-367-832A-34829
Query Match 37.1%; Score 10.4; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 16 CAGGAGTCCAG 27
DB 2 CAGGTAGTCCAG 13
RESULT 184
PCT-US02-25940-12401
; Sequence 12401, Application PC/TUS0225940
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25940
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 12401
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (1491220)...(1491234)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 145(
PCT-US02-25940-12401
Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 11 GTGTACAGGAGTCC 25
DB 1 GCGTGCAGGCGTCC 15
RESULT 185
PCT-US02-25940-14568
; Sequence 14568, Application PC/TUS0225940
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25940
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 14568
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (1754821)...(1754835)
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; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 17012
PCT-US02-25940-14568

Query Match      36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CGGGCCCTACGTGTA 15
      ||||| ||||| |||||
Db      1 CGGGCGGACGTGCA 15

RESULT 186
PCT-US02-25943-6183
; Sequence 6183, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 6183
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (542693)...(542707)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 6608
PCT-US02-25943-6183

Query Match      36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      14 TACAGGGAGTCCAGG 28
      ||||| ||||| |||||
Db      1 TCGAGGGCGTGCAGG 15

RESULT 187
PCT-US02-25943-27773
; Sequence 27773, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 27773
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (2698124)...(2698138)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 29757
PCT-US02-25943-27773

Query Match      36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      12 TGTACAGGGAGTCCA 26
      ||||| ||||| |||||
Db      1 TGTAGAGGCGTCCA 15

RESULT 188
PCT-US02-25943-31162/c
; Sequence 31162, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 31162
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3030196)...(3030210)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 3336
PCT-US02-25943-31162

Query Match      36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CGGGCCCTACGTGTA 15
      ||||| ||||| |||||
Db      15 CGGGCGCTTCGTGGA 1

RESULT 189
PCT-US02-25943-31163/c
; Sequence 31163, Application PC/TUS0225943
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: PCT/US02/25943
; CURRENT FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 31163
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3030196)...(3030210)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 3336
PCT-US02-25943-31163

Query Match      36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CGGGCCCTACGTGTA 15
      ||||| ||||| |||||
Db      15 CGGGCGCTTCGTGGA 1

RESULT 190
US-09-406-643-897/c
; Sequence 897, Application US/09406643
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Ludwig, Janos
; APPLICANT: Sproat, Brian
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: Compositions Having RNA Cleaving Activity
; FILE REFERENCE: MBH00-874-A (237/197)
; CURRENT APPLICATION NUMBER: US/09/406,643
; CURRENT FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 08/879,078
; PRIOR FILING DATE: 1997-06-19
; PRIOR APPLICATION NUMBER: US 08/878,640
; PRIOR FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 2606
; SOFTWARE: PatentIn version 3.0
```

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; SEQ ID NO 897
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-406-643-897

Query Match      36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 TACAGGGAGTCCAGG 28
DB 15 TCCTGGGAGCCAGG 1

RESULT 191
US-09-498-824A-897/c
; Sequence 897, Application US/09458824A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Ludwig, Janos
; APPLICANT: Sprout, Brian
; APPLICANT: Beigelman, Leo
; TITLE OF INVENTION: Compositions Having RNA Cleaving Activity
; FILE REFERENCE: MHB00-874-D (247/280)
; CURRENT APPLICATION NUMBER: US/09/498,824A
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 09/406,643
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 08/878,640
; PRIOR FILING DATE: 1997-06-19
; PRIOR APPLICATION NUMBER: US 08/879,078
; PRIOR FILING DATE: 1997-06-19
; NUMBER OF SEQ ID NOS: 3516
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 897
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-498-824A-897

Query Match      36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 TACAGGGAGTCCAGG 28
DB 15 TCCTGGGAGCCAGG 1

RESULT 192
US-09-611-577-21/c
; Sequence 21, Application US/09611577
; GENERAL INFORMATION:
; APPLICANT: Kazemi, Amir
; APPLICANT: Koshiy, Beena
; APPLICANT: Duda, Amy
; APPLICANT: Genaisance Pharmaceuticals
; TITLE OF INVENTION: Drug Target Isozymes: Polymorphisms in the G
; FILE REFERENCE: MMH-567US
; CURRENT APPLICATION NUMBER: US/09/611,577
; CURRENT FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-611-577-21

Query Match      36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 TACAGGGAGTCCAGG 28
DB 15 TCCTGGGAGCCAGG 1

RESULT 193
US-09-879-813-73/c
; Sequence 73, Application US/09879813
; GENERAL INFORMATION:
; APPLICANT: Sale, Julian E.
; APPLICANT: Neuberger, Michael S.
; APPLICANT: Cumbers, Sarah J.
; TITLE OF INVENTION: Method of Generating Diversity
; FILE REFERENCE: 18396/2005
; CURRENT APPLICATION NUMBER: US/09/879,813
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/828,717
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/GB99/03358
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)..(10)
; OTHER INFORMATION: E264
; OTHER INFORMATION: The sequence ACA replaces the sequence GAGAG.46bp.CGTC
US-09-879-813-73

Query Match      36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCCCTACGTGTACAG 18
DB 15 GCCCATGTGCACAG 1

RESULT 194
US-09-912-673A-55/c
; Sequence 55, Application US/09912673A
; GENERAL INFORMATION:
; APPLICANT: Ye, Bangce
; TITLE OF INVENTION: MEDIUM AND LOW DENSITY GENE CHIPS
; FILE REFERENCE: JNB 100
; CURRENT APPLICATION NUMBER: US/09/912,673A
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 15
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: P(qs)1 DNA probe
US-09-912-673A-55

Query Match      36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTACAGGGAGTC 24
DB 15 CTGTCCAGGGAGGC 1

RESULT 195
```

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US-10-146-505-73/c
; Sequence 73, Application US/10146505
; GENERAL INFORMATION:
; APPLICANT: Sale, Julian E.
; APPLICANT: Neuberger, Michael S.
; APPLICANT: Cumbers, Sarah J.
; TITLE OF INVENTION: Method of Generating Diversity
; FILE REFERENCE: 18396/2005B
; CURRENT APPLICATION NUMBER: US/10/146,505
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/828,717
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 09/879,813
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: PCT/GB99/03358
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: GB 9822104.7
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: GB 9901141.3
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: GB 9913435.5
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(10)
; OTHER INFORMATION: F264
; OTHER INFORMATION: The sequence ACA replaces the sequence GAGAG.46bp.CGTC
US-10-146-505-73

Query Match          36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4  GCCTACGTGTACAG 18
        ||||| |||||
Db      15  GCCCATGTGCACAG 1

RESULT 196
US-10-227-563-12401, Application US/10227563
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,563
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 12401
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (1491220)...(1491234)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 14502
US-10-227-563-12401

Query Match          36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      11  GTGTACAGGAGTCC 25
        ||||| |||||
Db      1  GCGTGAGGGGTCC 15

US-10-146-505-73/c
; Sequence 73, Application US/10146505
; GENERAL INFORMATION:
; APPLICANT: Sale, Julian E.
; APPLICANT: Neuberger, Michael S.
; APPLICANT: Cumbers, Sarah J.
; TITLE OF INVENTION: Method of Generating Diversity
; FILE REFERENCE: 18396/2005B
; CURRENT APPLICATION NUMBER: US/10/146,505
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/828,717
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 09/879,813
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: PCT/GB99/03358
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: GB 9822104.7
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: GB 9901141.3
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: GB 9913435.5
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(10)
; OTHER INFORMATION: F264
; OTHER INFORMATION: The sequence ACA replaces the sequence GAGAG.46bp.CGTC
US-10-146-505-73

Query Match          36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4  GCCTACGTGTACAG 18
        ||||| |||||
Db      15  GCCCATGTGCACAG 1

RESULT 196
US-10-227-563-12401, Application US/10227563
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,563
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 12401
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (1491220)...(1491234)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 14502
US-10-227-563-12401

Query Match          36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      11  GTGTACAGGAGTCC 25
        ||||| |||||
Db      1  GCGTGAGGGGTCC 15

US-10-227-563-14568, Application US/10227563
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,563
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 14568
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (1754821)...(1754835)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 1701
US-10-227-563-14568

Query Match          36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1  CGGGCCCTACGTGTA 15
        ||||| |||||
Db      1  CGGGCGCGACGTGCA 15

RESULT 197
US-10-227-563-14568, Application US/10227563
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,563
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 14568
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (1754821)...(1754835)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 1701
US-10-227-563-14568

Query Match          36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1  CGGGCCCTACGTGTA 15
        ||||| |||||
Db      1  CGGGCGCGACGTGCA 15

RESULT 198
US-10-227-565-6183, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 6183
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (542693)...(542707)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 66(
US-10-227-565-6183

Query Match          36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      14  TACAGGAGTCCAGG 28
        ||||| |||||
Db      1  TGCAGGGCGTGCAGG 15

RESULT 199
US-10-227-565-27773, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 27773
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.

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; FEATURE:
; LOCATION: (2698124)...(2698138)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 29757
US-10-227-565-27773
Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 12 TGTACAGGGAGTCCA 26
Db 1 TGTACAGGGAGTCCA 15
RESULT 200
US-10-227-565-31162/c
; Sequence 31162, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 31162
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3030196)...(3030210)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 33366
US-10-227-565-31162
Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CGGGCCCTACGTGA 15
Db 15 CGGGCGCTTCGTGA 1
RESULT 201
US-10-227-565-31163/c
; Sequence 31163, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 31163
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3030196)...(3030210)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 33365
US-10-227-565-31163
Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CGGGCCCTACGTGA 15
Db 15 CGGGCGCTTCGTGA 1
RESULT 202
US-10-227-565-31164/c
; Sequence 31164, Application US/10227565
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/227,565
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 31164
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3030196)...(3030210)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 33364
US-10-227-565-31164
Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CGGGCCCTACGTGA 15
Db 15 CGGGCGCTTCGTGA 1
RESULT 203
US-10-287-787-16397/c
; Sequence 16397, Application US/10287787
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Caulobacter crescentus complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,787
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 27958
; SOFTWARE: Proprietary
; SEQ ID NO 16397
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Caulobacter crescentus complete genome.
; FEATURE:
; LOCATION: (2480655)...(2480669)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 181
US-10-287-787-16397
Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 13 GTACAGGGAGTCCAG 27
Db 1 GTTCAGCGAGGCCAG 15
RESULT 204
US-10-287-787-25557/c
; Sequence 25557, Application US/10287787
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Caulobacter crescentus complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,787
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 27958
; SOFTWARE: Proprietary
; SEQ ID NO 25557
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Caulobacter crescentus complete genome.
; FEATURE:
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Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGGGCCCTACGTGTA 15
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Db 15 CGGGCGCTTCGTGGA 1

RESULT 210
US-10-367-832A-31163/c
; Sequence 31163, Application US/10367832A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367-832A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 64158
; SOFTWARE: Proprietary
; SEQ ID NO 31163
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
; FEATURE:
; LOCATION: (3030196)...(3030210)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 33365
US-10-367-832A-31163

Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGGGCCCTACGTGTA 15
    ||||| |||||
Db 15 CGGGCGCTTCGTGGA 1

RESULT 211
US-10-367-892-12401
; Sequence 12401, Application US/10367892
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/367-892
; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 25502
; SOFTWARE: Proprietary
; SEQ ID NO 12401
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, Plasmid
; FEATURE:
; LOCATION: (1491220)...(1491234)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 14502
US-10-367-892-12401

Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 11 GTGTACAGGAGTCC 25
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Db 1 CGGTGACAGGCGTCC 15

RESULT 212
US-10-367-892-14568
; Sequence 14568, Application US/10367892
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Deinococcus radiodurans R1 complete genome, Plasmid
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
US-10-367-892-14568

Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGGGCCCTACGTGTA 15
    ||||| |||||
Db 15 CGGGCGCTTCGTGGA 1

RESULT 213
US-10-453-850-897/c
; Sequence 897, Application US/10453850
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Ludwig, Janos
; APPLICANT: Sproat, Brian
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: Compositions Having RNA Cleaving Activity
; FILE REFERENCE: MBH00-874-A (237/197)
; CURRENT APPLICATION NUMBER: US/10/453,850
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: US/09/406,643
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 08/879,078
; PRIOR FILING DATE: 1997-06-19
; PRIOR APPLICATION NUMBER: US 08/878,640
; PRIOR FILING DATE: 1997-06-19
; NUMBER OF SEQ ID NOS: 2606
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 897
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-453-850-897

Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 TACAGGAGTCCAGG 28
    ||||| |||||
Db 15 TCCTGGGAGGCCAGG 1

Search completed: April 19, 2004, 15:45:30
Job time : 1 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2004, 15:06:48 ; Search time 0.001 Seconds
(without alignments)

116.984 Million cell updates/sec

Title: US-10-024-396-3-COPY

Perfect score: 28

Sequence: 1 cggccctacgtacagggagtcagg 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 180 seqs, 2089 residues

Total number of hits satisfying chosen parameters: 360

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 218 summaries

Database : issdb:* *Issued - Patents - NA*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	14.2	50.7	21	1	US-08-702-665A-19
2	13.4	47.9	18	1	US-08-633-792A-6
3	13.4	47.9	18	1	US-09-075-717A-6
4	12.4	44.3	19	1	US-08-630-592-18
5	12.4	44.3	19	1	US-08-714-991-18
6	12.4	44.3	19	1	US-09-032-365A-30
7	12.2	43.6	18	1	US-08-117-952-129
8	12.2	43.6	18	1	US-08-970-269A-6
9	12.2	43.6	18	1	US-08-474-177-23
10	11.2	40.0	16	1	US-08-487-033-23
11	11.2	40.0	16	1	US-08-480-810-23
12	11.2	40.0	16	1	US-08-508-735-23
13	11.2	40.0	16	1	US-08-848-251-23
14	11.2	40.0	16	1	US-08-486-047-23
15	11.2	40.0	16	1	US-09-120-130-23
16	11.2	40.0	16	1	US-09-115-252-23
17	11.2	40.0	16	1	US-08-988-515-23
18	11.2	40.0	16	1	US-09-120-148-23
19	11.2	40.0	16	1	US-09-120-149-23
20	11.2	40.0	16	1	US-09-201-139-23
21	11.2	40.0	16	1	US-09-120-131-23
22	11.2	40.0	16	1	US-08-182-968A-121
23	10.8	38.6	15	1	US-08-774-306A-121
24	10.8	38.6	15	1	US-09-064-156A-121
25	10.8	38.6	15	1	US-09-081-646-121
26	10.8	38.6	15	1	US-09-180-437-185
27	10.4	37.1	15	1	US-08-182-968A-297
28	10	35.7	15	1	US-08-319-492B-24
29	10	35.7	15	1	US-08-774-306A-297
30	10	35.7	15	1	US-09-064-156A-297
31	10	35.7	15	1	US-09-698-505A-38
32	9.8	35.0	15	1	US-08-182-968A-115
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34	9.8	35.0	15	1	US-08-774-306A-115
35	9.8	35.0	15	1	US-09-064-156A-115
36	9.8	35.0	15	1	US-09-180-437-184
37	9.8	35.0	15	1	PCT-US93-02612-2
38	9.4	33.6	12	1	US-09-203-231B-67
39	9.4	33.6	12	1	5174962-2
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41	9.2	32.9	14	1	US-08-623-891-20
42	9.2	32.9	14	1	US-09-340-861-20
43	9.2	32.9	14	1	US-09-634-262-20
44	9	32.1	12	1	US-08-494-301A-6
45	8.8	31.4	12	1	US-09-203-231B-67
46	8.8	31.4	12	1	US-09-281-418-211
47	8.8	31.4	13	1	US-09-014-304-3
48	8.8	31.4	13	1	US-09-874-601-30
49	8.4	30.0	10	1	US-08-192-942-7
50	8.4	30.0	10	1	US-08-777-266A-85
51	8.4	30.0	10	1	US-09-326-188B-85
52	8.4	30.0	10	1	US-09-769-482-14
53	8.4	30.0	11	1	US-08-777-266A-86
54	8.4	30.0	11	1	US-09-326-186B-86
55	8.4	30.0	11	1	US-09-249-155A-45
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58	8.4	30.0	12	1	US-08-777-266A-87
59	8.4	30.0	12	1	US-09-281-418-107
60	8.4	30.0	12	1	US-09-626-929-25
61	8.4	30.0	12	1	US-09-326-186B-87
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63	8.4	30.0	12	1	US-09-408-392-25
64	8.4	30.0	12	1	US-09-626-930-25
65	8.4	30.0	12	1	US-09-626-930-25
66	8.4	30.0	12	1	US-09-340-861-39
67	8.4	30.0	12	1	US-09-634-262-39
68	8.4	30.0	12	1	US-09-626-595-25
69	8.4	30.0	12	1	US-09-694-863-25
70	8.2	29.3	21	1	US-08-702-665A-19
71	8	28.6	9	1	US-09-989-789-2038
72	8	28.6	9	1	US-09-989-789-2100
73	8	28.6	9	1	US-09-989-789-2195
74	8	28.6	9	1	US-09-989-789-2453
75	8	28.6	9	1	US-09-989-789-2454
76	8	28.6	10	1	US-08-170-095B-12
77	8	28.6	10	1	US-08-396-866-12
78	8	28.6	11	1	US-09-301-721A-12
79	8	28.6	11	1	US-09-192-707-9
80	8	28.6	12	1	US-08-086-410-4
81	8	28.6	12	1	US-07-939-501A-17
82	8	28.6	12	1	US-08-025-038-15
83	7.8	27.9	11	1	US-09-249-155A-236
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85	7.8	27.9	11	1	PCT-US93-05668-4
86	7.8	27.9	12	1	US-08-035-928-19
87	7.8	27.9	12	1	US-08-435-350-107
88	7.8	27.9	12	1	US-08-494-301A-25
89	7.8	27.9	12	1	US-09-281-418-25
90	7.8	27.9	12	1	US-09-528-404-9
91	7.8	27.9	12	1	US-08-717-526-61
92	7.4	26.4	9	1	US-09-153-242-30
93	7.4	26.4	10	1	US-07-651-710A-33
94	7.4	26.4	10	1	US-08-074-879-3
95	7.4	26.4	10	1	US-08-468-057A-3
96	7.4	26.4	10	1	US-08-378-986-6
97	7.4	26.4	10	1	US-08-388-353-495
98	7.4	26.4	10	1	US-08-388-353-496
99	7.4	26.4	10	1	US-08-388-353-657
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101	7.4	26.4	10	1	US-08-388-353-661
102	7.4	26.4	10	1	US-08-388-353-662
103	7.4	26.4	10	1	US-08-488-551B-495
104	7.4	26.4	10	1	US-08-488-551B-496
105	7.4	26.4	10	1	US-08-488-551B-496
106	7.4	26.4	10	1	US-08-488-551B-496

C 107	7.4	26.4	10	1	US-08-488-551B-657	Sequence 657, App
C 108	7.4	26.4	10	1	US-08-488-551B-658	Sequence 658, App
C 109	7.4	26.4	10	1	US-08-488-551B-661	Sequence 661, App
C 110	7.4	26.4	10	1	US-08-488-551B-662	Sequence 662, App
C 111	7.4	26.4	10	1	US-08-488-551B-813	Sequence 813, App
C 112	7.4	26.4	10	1	US-08-488-551B-814	Sequence 814, App
C 113	7.4	26.4	10	1	US-08-522-384-34	Sequence 34, Appl
C 114	7.4	26.4	10	1	US-08-488-551B-12	Sequence 12, Appl
C 115	7.4	26.4	10	1	US-08-154-750A-17	Sequence 17, Appl
C 116	7.4	26.4	10	1	US-08-154-750A-37	Sequence 37, Appl
C 117	7.4	26.4	10	1	US-08-462-561B-26	Sequence 26, Appl
C 118	7.4	26.4	10	1	US-08-301-721A-27	Sequence 27, Appl
C 119	7.4	26.4	10	1	US-08-508-753B-160	Sequence 160, App
C 120	7.4	26.4	10	1	US-08-789-482-18	Sequence 18, Appl
C 121	7.4	26.4	10	1	US-08-504-132-10	Sequence 10, Appl
C 122	7.4	26.4	10	1	US-08-989-789-1630	Sequence 1630, App
C 123	7.4	26.4	10	1	US-08-989-789-1631	Sequence 1631, App
C 124	7.4	26.4	11	1	US-07-951-715A-55	Sequence 55, Appl
C 125	7.4	26.4	11	1	US-08-459-448A-55	Sequence 55, Appl
C 126	7.4	26.4	11	1	US-08-459-595A-55	Sequence 55, Appl
C 127	7.4	26.4	11	1	US-08-459-504B-55	Sequence 55, Appl
C 128	7.4	26.4	11	1	US-08-459-444-55	Sequence 55, Appl
C 129	7.4	26.4	11	1	US-08-547-422-55	Sequence 55, Appl
C 130	7.4	26.4	11	1	US-09-153-242-39	Sequence 39, Appl
C 131	7.4	26.4	11	1	US-09-249-155A-61	Sequence 61, Appl
C 132	7.4	26.4	11	1	US-09-249-155A-162	Sequence 162, App
C 133	7.4	26.4	11	1	US-09-249-155A-203	Sequence 203, App
C 134	7.4	26.4	11	1	US-09-249-155A-231	Sequence 231, App
C 135	7.4	26.4	18	1	US-08-633-792A-6	Sequence 6, Appl
C 136	7.4	26.4	18	1	US-09-075-717A-6	Sequence 6, Appl
C 137	7.2	25.7	11	1	US-08-327-525A-35	Sequence 35, Appl
C 138	7.2	25.7	11	1	US-08-531-137B-35	Sequence 35, Appl
C 139	7.2	25.7	11	1	US-09-159-765-35	Sequence 35, Appl
C 140	7.2	25.7	11	1	US-09-796-071-35	Sequence 35, Appl
C 141	7.2	25.7	12	1	US-09-281-418-107	Sequence 107, Appl
C 142	7.2	25.7	12	1	US-09-281-418-25	Sequence 25, Appl
C 143	7.2	25.7	15	1	US-08-182-968A-297	Sequence 297, App
C 144	7.2	25.7	15	1	US-08-774-306A-297	Sequence 297, App
C 145	7.2	25.7	15	1	US-09-064-156A-297	Sequence 297, App
C 146	7	25.0	8	1	US-08-859-954-179	Sequence 179, App
C 147	7	25.0	8	1	US-08-859-954-289	Sequence 289, App
C 148	7	25.0	8	1	US-08-859-954-436	Sequence 436, App
C 149	7	25.0	8	1	US-08-859-954-437	Sequence 437, App
C 150	7	25.0	8	1	US-08-859-954-510	Sequence 510, App
C 151	7	25.0	8	1	US-08-878-693-5	Sequence 5, Appl
C 152	7	25.0	9	1	US-08-331-398A-37	Sequence 37, Appl
C 153	7	25.0	9	1	US-08-605-163-11	Sequence 11, Appl
C 154	7	25.0	9	1	US-08-605-163-12	Sequence 12, Appl
C 155	7	25.0	9	1	US-08-331-397B-37	Sequence 37, Appl
C 156	7	25.0	9	1	US-08-759-804A-37	Sequence 37, Appl
C 157	7	25.0	9	1	US-09-046-858A-3	Sequence 3, Appl
C 158	7	25.0	9	1	US-09-227-693-37	Sequence 37, Appl
C 159	7	25.0	9	1	US-09-153-242-33	Sequence 33, Appl
C 160	7	25.0	9	1	US-09-989-789-2121	Sequence 2121, App
C 161	7	25.0	9	1	US-09-989-789-2122	Sequence 2122, App
C 162	7	25.0	9	1	US-09-989-789-2330	Sequence 2330, App
C 163	7	25.0	9	1	US-09-989-789-2331	Sequence 2331, App
C 164	7	25.0	9	1	US-09-989-789-2347	Sequence 2347, App
C 165	7	25.0	9	1	US-09-989-789-2348	Sequence 2348, App
C 166	7	25.0	9	1	US-09-450-513-3	Sequence 3, Appl
C 167	7	25.0	10	1	US-09-263-790-19	Sequence 19, Appl
C 168	7	25.0	10	1	US-09-538-341-12	Sequence 12, Appl
C 169	7	25.0	10	1	US-09-785-716A-18	Sequence 18, Appl
C 170	7	25.0	10	1	US-09-799-880-19	Sequence 19, Appl
C 171	7	25.0	10	1	US-08-590-571-19	Sequence 19, Appl
C 172	7	25.0	10	1	US-08-590-571-31	Sequence 31, Appl
C 173	7	25.0	10	1	US-08-388-353-659	Sequence 659, App
C 174	7	25.0	10	1	US-08-388-353-660	Sequence 660, App
C 175	7	25.0	10	1	US-08-468-856B-14	Sequence 14, Appl
C 176	7	25.0	10	1	US-08-488-551B-659	Sequence 659, App
C 177	7	25.0	10	1	US-08-488-551B-660	Sequence 660, App
C 178	7	25.0	10	1	US-08-468-856A-14	Sequence 14, Appl
C 179	7	25.0	10	1	US-08-906-691-10	Sequence 10, Appl

C 180	7	25.0	10	1	US-08-522-384-27	Sequence 27, Appl
C 181	7	25.0	10	1	US-09-154-750A-49	Sequence 49, Appl
C 182	7	25.0	10	1	US-09-313-221A-136	Sequence 136, App
C 183	7	25.0	10	1	US-09-537-186-13	Sequence 13, Appl
C 184	7	25.0	10	1	US-09-508-753B-151	Sequence 151, App
C 185	7	25.0	10	1	US-10-042-111-31	Sequence 31, Appl
C 186	7	25.0	10	1	US-09-538-456-9	Sequence 9, Appl
C 187	7	25.0	10	1	US-09-769-482-43	Sequence 43, Appl
C 188	7	25.0	10	1	US-09-989-789-1385	Sequence 1285, App
C 189	7	25.0	10	1	US-09-989-789-1307	Sequence 1307, App
C 190	7	25.0	10	1	US-09-989-789-1314	Sequence 1314, App
C 191	6.8	24.3	10	1	US-09-263-790-19	Sequence 19, Appl
C 192	6.8	24.3	10	1	US-09-538-341-12	Sequence 12, Appl
C 193	6.8	24.3	10	1	US-09-785-716A-18	Sequence 18, Appl
C 194	6.8	24.3	10	1	US-09-799-880-19	Sequence 19, Appl
C 195	6.8	24.3	10	1	US-08-388-353-660	Sequence 660, App
C 196	6.8	24.3	10	1	US-08-488-551B-660	Sequence 660, App
C 197	6.8	24.3	10	1	US-09-537-186-13	Sequence 13, Appl
C 198	6.8	24.3	10	1	US-09-538-456-9	Sequence 9, Appl
C 199	6.6	23.6	16	1	US-08-474-177-23	Sequence 23, Appl
C 200	6.6	23.6	16	1	US-08-487-033-23	Sequence 23, Appl
C 201	6.6	23.6	16	1	US-08-480-810-23	Sequence 23, Appl
C 202	6.6	23.6	16	1	US-08-508-735-23	Sequence 23, Appl
C 203	6.6	23.6	16	1	US-08-848-251-23	Sequence 23, Appl
C 204	6.6	23.6	16	1	US-08-486-047-23	Sequence 23, Appl
C 205	6.6	23.6	16	1	US-09-120-130-23	Sequence 23, Appl
C 206	6.6	23.6	16	1	US-09-115-252-23	Sequence 23, Appl
C 207	6.6	23.6	16	1	US-08-986-515-23	Sequence 23, Appl
C 208	6.6	23.6	16	1	US-09-120-128-23	Sequence 23, Appl
C 209	6.6	23.6	16	1	US-09-120-129-23	Sequence 23, Appl
C 210	6.6	23.6	16	1	US-09-201-139-23	Sequence 23, Appl
C 211	6.6	23.6	16	1	US-09-120-131-23	Sequence 23, Appl
C 212	6.4	22.9	10	1	US-08-522-384-34	Sequence 34, Appl
C 213	6.4	22.9	10	1	US-09-425-798-12	Sequence 12, Appl
C 214	6.2	22.1	15	1	US-08-319-492B-24	Sequence 24, Appl
C 215	6	21.4	9	1	US-09-989-789-2453	Sequence 2453, App
C 216	6	21.4	9	1	US-09-989-789-2454	Sequence 2454, App
C 217	6	21.4	9	1	US-09-153-242-30	Sequence 30, Appl
C 218	6	21.4	9	1	US-09-153-242-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1

US-08-702-665A-19

Sequence 19, Application US/08702665A

Patent No. 6274708

GENERAL INFORMATION:

APPLICANT: Hilton, Douglas J.

TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSER: SCULLY, SCOTT, MURPHY & PRESSER

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: United States of America

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/702.665A

FILING DATE: 20-DEC-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Presser, Leopold

REGISTRATION NUMBER: 19,827

REFERENCE/DOCKET NUMBER: 10296

TELECOMMUNICATION INFORMATION:

STREET: 3400 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,592

FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J.
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: A59504/BIR/PJS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 7811989
TELEFAX: (415) 3983249
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
US-08-630-592-18

Query Match 44.3%; Score 12.4; DB 1; Length 19;
Best Local Similarity 92.9%; Pred. No. 10;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGGAGTCCAGG 28
|||||
DB 6 ACAGGGAGACCAGG 19

RESULT 5
US-08-714-991-18
Sequence 18, Application US/08714991
Patent No. 5776762
GENERAL INFORMATION:
APPLICANT: NORTON, Michael
APPLICANT: NISHINA, Patsy
APPLICANT: NAGERT, Juergen
TITLE OF INVENTION: OBESITY ASSOCIATED GENES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,991
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SHERWOOD, Pamela J.
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: A-59504-1/PJS
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-494-8700
TELEFAX: 415-494-8771
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
US-08-714-991-18

Query Match 44.3%; Score 12.4; DB 1; Length 19;
Best Local Similarity 92.9%; Pred. No. 10;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGGAGTCCAGG 28
|||||
DB 6 ACAGGGAGACCAGG 19

RESULT 6
US-09-032-365A-30
Sequence 30, Application US/09032365A
Patent No. 6114502
GENERAL INFORMATION:
APPLICANT: No. 6114502th, Michael
APPLICANT: Nishina, Patsy
APPLICANT: Naggart, Juergen
TITLE OF INVENTION: GENE FAMILY ASSOCIATED WITH
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Boricevic & Reed, LLP
STREET: 285 Hamilton Avenue, Suite 200
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,365A
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J.
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEQ-2CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
TELEFAX: 650 327-3231
TELEX:
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-032-365A-30

Query Match 44.3%; Score 12.4; DB 1; Length 19;
Best Local Similarity 92.9%; Pred. No. 10;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGGAGTCCAGG 28
 |||||
 Db 6 ACAGGGAGTCCAGG 19

RESULT 7

US-08-117-952-129/c
 ; Sequence 129, Application US/08117952
 ; Patent No. 5851760
 ; GENERAL INFORMATION:
 ; APPLICANT: Evans, Glen A.
 ; TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
 ; TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
 ; NUMBER OF SEQUENCES: 797
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
 ; STREET: 444 South Flower Street, Suite 2000
 ; CITY: Los Angeles
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 90071

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/117,952
 FILING DATE: 07-SEP-1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/078,471
 FILING DATE: 15-JUN-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Reiter, Stephen E.
 REGISTRATION NUMBER: 31,192
 REFERENCE/DOCKET NUMBER: P41 9423
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-546-4737
 TELEFAX: 619-546-9392
 INFORMATION FOR SEQ ID NO: 129:

SEQUENCE CHARACTERISTICS:
 LENGTH: 18 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLESCULE TYPE: Oligonucleotide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO

Query Match 43.6%; Score 12.2; DB 1; Length 18;
 Best Local Similarity 82.4%; Pred. No. 10;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 11 GTGTACAGGAGTCCAG 27
 |||||
 Db 18 GTGGAAGGAGTCCGG 2

RESULT 8

US-08-970-269A-6
 ; Sequence 6, Application US/08970269A
 ; Patent No. 5976803
 ; GENERAL INFORMATION:
 ; APPLICANT: Kathryn Meek
 ; TITLE OF INVENTION: Genetic Test For Equine Severe
 ; TITLE OF INVENTION: Combined Immunodeficiency Disease
 ; NUMBER OF SEQUENCES: 32
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dr. Benjamin A. Adler

STREET: 8011 Candle Lane
 CITY: Houston
 STATE: Texas
 COUNTRY: USA
 ZIP: 77071

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple
 OPERATING SYSTEM: Macintosh
 SOFTWARE: Microsoft Word for Macintosh
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/970,269A
 FILING DATE: No. 5976803ember 14, 1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Adler Ph.D., Benjamin A.
 REGISTRATION NUMBER: 35,423
 REFERENCE/DOCKET NUMBER: D5860
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 713-777-2321
 TELEFAX: 713-777-6908
 INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
 LENGTH: 18
 TYPE: nucleic acid
 STRANDEDNESS: double stranded
 TOPOLOGY: linear
 MOLESCULE TYPE: other nucleic acid
 DESCRIPTION: no
 HYPOTHETICAL: no
 ANTI-SENSE: no
 ORIGINAL SOURCE:
 FEATURE:

US-08-970-269A-6

Query Match 43.6%; Score 12.2; DB 1; Length 18;
 Best Local Similarity 82.4%; Pred. No. 10;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 TGTACAGGAGTCCAGG 28
 |||||
 Db 1 TGTACAGGAGTCCAGG 17

RESULT 9

US-08-407-562-6
 ; Sequence 6, Application US/09407562
 ; Patent No. 6294334
 ; GENERAL INFORMATION:
 ; APPLICANT: Kathryn Meek
 ; TITLE OF INVENTION: Genetic Test For Equine Severe
 ; TITLE OF INVENTION: Combined Immunodeficiency Disease
 ; NUMBER OF SEQUENCES: 32
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dr. Benjamin A. Adler
 ; STREET: 8011 Candle Lane
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: USA
 ; ZIP: 77071

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple
 OPERATING SYSTEM: Macintosh
 SOFTWARE: Microsoft Word for Macintosh
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/407,562
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/970,269
 FILING DATE: No. 6294334ember 14, 1997
 CLASSIFICATION:

```
ATTORNEY/AGENT INFORMATION:
NAME: Adler Ph.D., Benjamin A.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5860
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 18
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: no
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
FEATURE:
US-09-407-562-6

Query Match 43.6%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 10;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 TCTACAGGAGTCCAGG 28
DB 1 TCTACAGGGAATTCAGG 17

RESULT 10
US-08-474-177-23
Sequence 23, Application US/08474177
Patent No. 5624819
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,177
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:

ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-474-177-23

Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 15;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGTCTACAGGAGTCC 25
DB 1 CGTCTCAGGAGGCC 16

RESULT 11
US-08-487-033-23
Sequence 23, Application US/08487033
Patent No. 5739027
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS1E1-Beta GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,033
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
```

NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-487-033-23

Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred.No.15;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTACAGGAGTCC 25
|||||
DB 1 CGGTCCAGGAGCCC 16

RESULT 12
US-08-480-810-23
Sequence 23, Application US/08480810
Patent No. 5801236
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS1 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480.810
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24884-109348
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-480-810-23
Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred.No.15;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 10 CGGTACAGGAGTCC 25
|||||
DB 1 CGGTCCAGGAGCCC 16
RESULT 13
US-08-508-735-23
Sequence 23, Application US/08508735
Patent No. 5843756
GENERAL INFORMATION:
APPLICANT: Stone, Steven
APPLICANT: Jiang, Ping
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/508,735
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US to be assigned
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO

ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-508-735-23

Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 15;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTGACAGGAGTCC 25
Db 1 CGGTGACAGGAGGCC 16

RESULT 14

US-08-848-251-23
Sequence 23, Application US/08848251
Patent No. 5989815

GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND
METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS
TITLE OF INVENTION: GENE
NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC

COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/848,251
FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/474,083
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994

ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-G

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-848-251-23

Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 15;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTGACAGGAGTCC 25
Db 1 CGGTGACAGGAGGCC 16

RESULT 15

US-08-486-047-23
Sequence 23, Application US/08486047
Patent No. 5994095

GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS2 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC

COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/486,047
FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994

ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-B

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-486-047-23

Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 15;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTACAGGAGTCC 25
|||||
Db 1 CGGTCCAGGAGCCC 16

RESULT 16

US-09-120-130-23
Sequence 23, Application US/09120130
Patent No. 6037462
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS1 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/120,130
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,810
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELEPHONE: 202-962-8300
TELEFAX: 202-962-4810

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO

ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-120-130-23

Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 15;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTACAGGAGTCC 25
|||||
Db 1 CGGTCCAGGAGCCC 16

RESULT 17

US-09-115-252-23
Sequence 23, Application US/09115252
Patent No. 6060301
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS1 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,252
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/480,810
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO

ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-115-252-23

Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred.No.15;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTACAGGAGTCC 25
| | | | | | | | | | | | | | | | | |
Db 1 CGGTCCAGGAGGCC 16

RESULT 18
US-08-986-515-23
Sequence 23, Application US/08986515
Patent No. 6090578

GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS1 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,515
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,810
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-8300
TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:

ORGANISM: Homo sapiens
US-08-986-515-23

Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred.No.15;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTACAGGAGTCC 25
| | | | | | | | | | | | | | | | | |
Db 1 CGGTCCAGGAGGCC 16

RESULT 19
US-09-120-128-23
Sequence 23, Application US/09120128
Patent No. 6140473

GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS2 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/120,128
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/486,047
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:

ORGANISM: Homo sapiens

Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 15;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTACAGGAGTCC 25
|||||
DB 1 CGGTCCAGGAGCCC 16

RESULT 20

US-09-120-129-23
; Sequence 23, Application US/09120129
; Patent No. 6180776

GENERAL INFORMATION:

APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS2 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/120,129
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,047
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24884-109348-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-962-8300

TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: YES

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 15;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTACAGGAGTCC 25
|||||
DB 1 CGGTCCAGGAGCCC 16

RESULT 21

US-09-201-139-23
; Sequence 23, Application US/09201139
; Patent No. 6210949

GENERAL INFORMATION:

APPLICANT: Stone, Steven
APPLICANT: Jiang, Ping
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,139
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/508,735
FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24884-109348

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-962-8300

TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: YES

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

US-09-201-139-23

Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 15;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTACAGGAGTCC 25
|||||
DB 1 CGGTCCAGGAGCCC 16

RESULT 22
US-09-120-131-23
; Sequence 23, Application US/09120131
; Patent No. 6218146
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS2 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/120,131
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/486,047
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-09-120-131-23

Query Match 40.0%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 15;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTGACGGAGTCC 25
Db 1 CGGTGACGGAGTCC 16

RESULT 23
US-08-182-968A-121
; Sequence 121, Application US/08182968A
; Patent No. 5610054
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,968A
; FILING DATE: 13-JANUARY-1994
; PRIOR APPLICATION DATA: 07/882,888
; APPLICATION NUMBER: 14-MAY-1992
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-182-968A-121

Query Match 38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 17;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCCCTACGTGTA 15
Db 1 GGGCCCTACGTGTA 14

RESULT 24
US-08-774-306A-121
; Sequence 121, Application US/08774306A
; Patent No. 5869253
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/774,306A
FILING DATE: December 26, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/182,968
FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/882,888
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Waiburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 227/227
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-774-306A-121

Query Match 38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 17;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCCCTACGTGTA 15
DB 1 GGGCCCUCCGUGCA 14

RESULT 25
US-09-064-156A-121
; Sequence 121, Application US/09064156A
; Patent No. 6132966
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 498
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,156A
FILING DATE: April 21, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/774,306
FILING DATE: December 26, 1996
APPLICATION NUMBER: 08/182,968
FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/882,888
FILING DATE: May 14, 1992

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/081,646
FILING DATE: December 26, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/182,968
FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/882,888
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Waiburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 234/083
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-064-156A-121

Query Match 38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 17;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCCCTACGTGTA 15
DB 1 GGGCCCUCCGUGCA 14

RESULT 26
US-09-081-646-637/c
; Sequence 637, Application US/09081646
; Patent No. 633152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 633152mal and
; FILE REFERENCE: 01107.74664
; CURRENT APPLICATION NUMBER: US/09/081,646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 637
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-081-646-637

Query Match 38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 ACAGGAGTCCAGG 28
DB 14 ACAGAGATCCATG 1

RESULT 27
US-09-180-437-185
; Sequence 185, Application US/09180437
; Patent No. 6251873
; GENERAL INFORMATION:
; APPLICANT: FUKUSAKO, Shioji
; APPLICANT: MORISAWA, Yoshifumi
; APPLICANT: KUSUYAMA, Takeshi
; TITLE OF INVENTION: Antisense Compounds to CD14
; FILE REFERENCE: 1110-209P
; CURRENT APPLICATION NUMBER: US/09/180,437
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: PCT/JP98/00953
; EARLIER FILING DATE: 1998-03-09
; EARLIER APPLICATION NUMBER: 09-053518 JAPAN
```

EARLIER FILING DATE: 1997-03-07
NUMBER OF SEQ ID NOS: 289
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 185
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: other nucleic acid
OTHER INFORMATION: acid
US-09-180-437-185

Query Match 37.1%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 23;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 17 AGGAGTCCAGG 28
|||||
DB 4 AGGAGTTCAGG 15

RESULT 28
US-08-182-968A-297
; Sequence 297, Application US/08182968A
; Patent No. 5610054
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,968A
; FILING DATE: 13-JANUARY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,888
; FILING DATE: 14-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 297:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-182-968A-297

Query Match 35.7%; Score 10; DB 1; Length 15;
Best Local Similarity 90.0%; Pred. No. 29;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGAGTCCAGG 28
|||||

Db 3 GGAGUCCAGG 12

RESULT 29
US-08-319-492B-24
; Sequence 24, Application US/08319492B
; Patent No. 5616488
; GENERAL INFORMATION:
; APPLICANT: Sullivan, Sean M.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF IL-5
; NUMBER OF SEQUENCES: 751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,492B
; FILING DATE: October 7, 1994
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/276
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-319-492B-24

Query Match 35.7%; Score 10; DB 1; Length 15;
Best Local Similarity 70.0%; Pred. No. 29;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCTACGTGTA 15
|||||

Db 5 CCUACGUGUA 14

RESULT 30
US-08-774-306A-297
; Sequence 297, Application US/08774306A
; Patent No. 5869253
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C

```
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,306A
; FILING DATE: December 26, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/182,968
; FILING DATE: January 13, 1994
; APPLICATION NUMBER: 07/882,888
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 213/227
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 297:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-774-306A-297

Query Match 35.7%; Score 10; DB 1; Length 15;
Best Local Similarity 90.0%; Pred. No. 29;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGAGTCCAGG 28
Db 3 GGAGUCCAGG 12

RESULT 31
US-09-064-156A-297
; Sequence 297, Application US/09064156A
; Patent No. 6132966
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 498
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/064,156A
; FILING DATE: April 21, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/774,306
; FILING DATE: December 26, 1996
; APPLICATION NUMBER: 08/182,968
; FILING DATE: January 13, 1994
; APPLICATION NUMBER: 07/882,888
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 234/083
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 297:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-064-156A-297

Query Match 35.7%; Score 10; DB 1; Length 15;
Best Local Similarity 90.0%; Pred. No. 29;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGAGTCCAGG 28
Db 3 GGAGUCCAGG 12

RESULT 32
US-09-698-505A-38/c
; Sequence 38, Application US/09698505A
; Patent No. 6479242
; GENERAL INFORMATION:
; APPLICANT: Guo, Baochuan
; TITLE OF INVENTION: A NO. 6479242 Method for Genotyping of Single Nucleotide Polym
; FILE REFERENCE: 27433/04001
; CURRENT APPLICATION NUMBER: US/09/698,505A
; CURRENT FILING DATE: 2001-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 14
; TYPE: DNA
; ORGANISM: A Homozygote
; US-09-698-505A-38

Query Match 35.0%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 29;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 TGTACAGGAGTC 24
Db 14 TGGCAGGAGTC 2

RESULT 33
US-08-182-968A-115
; Sequence 115, Application US/08182968A
; Patent No. 5610054
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
```


ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,968A
FILING DATE: 13-JANUARY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/882,888
FILING DATE: 14-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 205/277
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 115:

Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGTA 15
| | | | | :
Db 2 GCCCUAGUAUA 14

US-08-182-968A-115

SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-182-968A-115

Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGTA 15
| | | | | :
Db 2 GCCCUAGUAUA 14

US-08-182-968A-115

SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-182-968A-115

Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGTA 15
| | | | | :
Db 2 GCCCUAGUAUA 14

US-08-182-968A-115

SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-182-968A-115

Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGTA 15
| | | | | :
Db 2 GCCCUAGUAUA 14

US-08-182-968A-115

SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-182-968A-115

Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGTA 15
| | | | | :
Db 2 GCCCUAGUAUA 14

US-08-182-968A-115

SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-182-968A-115

Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGTA 15
| | | | | :
Db 2 GCCCUAGUAUA 14

US-08-182-968A-115

SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-182-968A-115

Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGTA 15
| | | | | :
Db 2 GCCCUAGUAUA 14

US-08-182-968A-115

SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-182-968A-115

Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGTA 15
| | | | | :
Db 2 GCCCUAGUAUA 14

US-08-182-968A-115

SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-182-968A-115

Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGTA 15
| | | | | :
Db 2 GCCCUAGUAUA 14

US-08-182-968A-115

SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-182-968A-115

Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGTA 15
| | | | | :
Db 2 GCCCUAGUAUA 14

US-08-182-968A-115

SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-182-968A-115

Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGTA 15
| | | | | :
Db 2 GCCCUAGUAUA 14

US-08-182-968A-115

SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-182-968A-115

Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGTA 15
| | | | | :
Db 2 GCCCUAGUAUA 14

US-08-182-968A-115

SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-182-968A-115

Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGTA 15
| | | | | :
Db 2 GCCCUAGUAUA 14

US-08-182-968A-115

SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-182-968A-115

Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGTA 15
| | | | | :
Db 2 GCCCUAGUAUA 14

US-08-182-968A-115

SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-182-968A-115

Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGTA 15
| | | | | :
Db 2 GCCCUAGUAUA 14

US-08-182-968A-115

SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-182-968A-115

Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGTA 15
| | | | | :
Db 2 GCCCUAGUAUA 14

US-08-182-968A-115

SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-182-968A-115

Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGTA 15
| | | | | :
Db 2 GCCCUAGUAUA 14

US-08-182-968A-115

SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-182-968A-115

Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGTA 15
| | | | | :
Db 2 GCCCUAGUAUA 14

US-08-182-968A-115

SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-182-968A-115

Query Match 35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGTA 15
| | | | | :
Db 2 GCCCUAGUAUA 14

US-08-182-968A-115

SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-182-968A

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-064-156A-115

Query Match      35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCCCTACGTGTA 15
   |||||:|:|:|
Db 2 GCCCUCAGUAUA 14

RESULT 36
US-09-180-437-134/c
; Sequence 134, Application US/09180437
; Patent No. 6251873
; GENERAL INFORMATION:
; APPLICANT: FUKUSAKO, Shioji
; APPLICANT: MORISAWA, Yoshifumi
; APPLICANT: KUSUYAMA, Takeshi
; TITLE OF INVENTION: Antisense Compounds to CD14
; FILE REFERENCE: 1110-209P
; CURRENT APPLICATION NUMBER: US/09/180,437
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: PCT/JP98/00953
; EARLIER FILING DATE: 1998-03-09
; EARLIER APPLICATION NUMBER: 09-053518 JAPAN
; EARLIER FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 134
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: other nucleic
; OTHER INFORMATION: acid
US-09-180-437-134

Query Match      35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 33;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCCCTACGTGT 14
   |||||:|:|:|
Db 13 GCGCCCTGCGTGT 1

RESULT 37
PCT-US93-02612-2/c
; Sequence 2, Application PC/TUS9302612
; GENERAL INFORMATION:
; APPLICANT: Cable, Michael
; APPLICANT: Hesson, Thomas
; APPLICANT: Mannarino, Anthony
; TITLE OF INVENTION: Monomeric Platelet-Derived Growth Factor and Prevention of
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: One Giralda Farms
; CITY: Madison
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07940
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 4.00B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/02612
```

```
; FILING DATE: 19930326
; CLASSIFICATION:
; PRIOR APPLICATION DATA: None
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul, G.
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: JB0255
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-822-7255
; TELEFAX: 201-822-7039
; TELEX: 219165
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US93-02612-2

Query Match      35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 33;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 CAGGGAGTCCAGG 28
   |||||:|:|:|
Db 15 CAGGGAACCCAGG 3

RESULT 38
US-09-203-231B-67
; Sequence 67, Application US/09203231B
; Patent No. 6355423
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan M
; APPLICANT: Nallur, Girish N
; APPLICANT: Hu, Xinghua
; TITLE OF INVENTION: Methods and Devices for Measuring
; TITLE OF INVENTION: Differential Gene Expression
; FILE REFERENCE: 7934-052
; CURRENT APPLICATION NUMBER: US/09/203,231B
; CURRENT FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 60/105,305
; PRIOR FILING DATE: 1997-12-03
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-203-231B-67

Query Match      33.6%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 27;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCTACGTGTAC 16
   |||||:|:|:|
Db 2 CCTACGTGTAC 12

RESULT 39
5174962-2
; Patent No. 5174962
; APPLICANT: BRENNAN, THOMAS M.
; TITLE OF INVENTION: APPARATUS FOR DETERMINING DNA SEQUENCES
; BY MASS SPECTROMETRY
; NUMBER OF SEQUENCES: 2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/459,728
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
```

; APPLICATION NUMBER: 209,247
; FILING DATE: 20-JUN-1988
; SEQ ID NO:2:
; LENGTH: 12
5174962-2

Query Match 33.6%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 27;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 ACGTGTACAGG 19
|||||
DB 1 ACGTGTACAG 11

RESULT 40
5174962-2/c
; Patent No. 5174962
; APPLICANT: BRENNAN, THOMAS M.
; TITLE OF INVENTION: APPARATUS FOR DETERMINING DNA SEQUENCES
; BY MASS SPECTROMETRY
; NUMBER OF SEQUENCES: 2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/459,728
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 209,247
; FILING DATE: 20-JUN-1988
; SEQ ID NO:2:
; LENGTH: 12
5174962-2

Query Match 33.6%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 27;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 ACGTGTACAGG 19
|||||
DB 12 ACGTGTACAG 2

RESULT 41
US-08-623-891-20/c
; Sequence 20, Application US/08623891
; Patent No. 5795778
; GENERAL INFORMATION:
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; OPERATING SYSTEM: INHIBITING HERPES SIMPLEX
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/623,891
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/238,200
; FILING DATE:
; APPLICATION NUMBER: US/07/987,133
; FILING DATE:
; APPLICATION NUMBER: 07/882,921

; FILING DATE: May 14, 1992
; APPLICATION NUMBER: 07/948,359
; FILING DATE: September 18, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 200/209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-623-891-20

Query Match 32.9%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 42;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGTGATCAGGGAGT 23
|||||
DB 14 CGTGATCAGGGAGT 1

RESULT 42
US-05-340-861-20/c
; Sequence 20, Application US/09340861
; Patent No. 6432704
; GENERAL INFORMATION:
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HERPES SIMPLEX
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/340,861
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/987,133
; FILING DATE:
; APPLICATION NUMBER: 07/882,921
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: 07/948,359
; FILING DATE: September 18, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 200/209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: nucleic acid

```
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-340-861-20

Query Match      32.9%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 42;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 CGGTACAGGAGT 23
Db 14 CGTGATCAGGGCGT 1

RESULT 43
US-09-634-262-20/c
; Sequence 20, Application US/09634262
; Patent No. 6440719
; GENERAL INFORMATION:
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HERPES SIMPLEX
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/634,262
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/987,133
; FILING DATE:
; APPLICATION NUMBER: 07/882,921
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: 07/948,359
; FILING DATE: September 18, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 200/209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-634-262-20

Query Match      32.9%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 42;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 CGGTACAGGAGT 23
Db 14 CGTGATCAGGGCGT 1

RESULT 44
US-08-494-301A-6/c
; Sequence 6, Application US/08494301A
; Patent No. 5856461
; GENERAL INFORMATION:
; APPLICANT: Colote, Soudhir
; APPLICANT: Pirotzky, Eduardo
; TITLE OF INVENTION: Oligonucleotides to Inhibit the
; TITLE OF INVENTION: Expression of Isoprenyl Protein Transferases
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lucas & Just
; STREET: 205 E. 42nd Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch,
; MEDIUM TYPE: 1.44 MB storage
; COMPUTER: IBM 486 Compatible
; OPERATING SYSTEM: MS-DOS 5.0
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,301A
; FILING DATE: 23-JUNE-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9413035.8
; FILING DATE: 29-JUNE-1994
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleotide
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: Yes
US-08-494-301A-6

Query Match      32.1%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 GTACAGGGA 21
Db 12 GTACAGGGA 4

RESULT 45
US-09-203-231B-67/c
; Sequence 67, Application US/09203231B
; Patent No. 6355423
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan M
; APPLICANT: Nallur, Girish N
; APPLICANT: Hu, Xinghua
; TITLE OF INVENTION: Methods and Devices for Measuring
; TITLE OF INVENTION: Differential Gene Expression
; FILE REFERENCE: 7934-052
; CURRENT APPLICATION NUMBER: US/09/203,231B
; CURRENT FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 60/105,305
; PRIOR FILING DATE: 1997-12-03
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-203-231B-67

Query Match      31.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 40;
```

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Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 13 GTACAGGAGTC 24
DB 12 GTACAGGTAGC 1

RESULT 46
US-09-281-418-211/c
; Sequence 211, Application US/09281418
; Patent No. 6287769
; GENERAL INFORMATION:
; APPLICANT: Inoue, Takakazu
; TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA F
; TITLE OF INVENTION: agent, Method of Assaying Microorganisms, Method of Analyzing Mi
; TITLE OF INVENTION: nisms and Method of Assaying Contaminant
; FILE REFERENCE: 9982-7
; CURRENT APPLICATION NUMBER: US/09/281.418
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: JP/1998/87651
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: JP/1999/69694
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 216
; SEQ ID NO 211
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Primer
; OTHER INFORMATION: Primer
US-09-281-418-211

Query Match 31.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 40;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 CCTACGTGTAC 16
DB 12 CCATACGTGCAC 1

RESULT 47
US-09-014-304-3
; Sequence 3, Application US/09014304
; Patent No. 6063573
; GENERAL INFORMATION:
; APPLICANT: Kayem, Jon Paiz
; TITLE OF INVENTION: Cycling Probe Technology Using Electron Transfer
; TITLE OF INVENTION: Detection
; FILE REFERENCE: A65687/RFT/RMS/RVK
; CURRENT APPLICATION NUMBER: US/09/014,304
; CURRENT FILING DATE: 1998-01-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-014-304-3

Query Match 31.4%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 47;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 9 ACGTGACAGG 20
DB 1 ACGTGCCATGG 12

RESULT 48
US-09-874-601-30

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; Sequence 30, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHC
; TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/874,601
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 30
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(7)
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-30

Query Match 31.4%; Score 8.8; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 CGGGCCCTACGT 12
DB 1 CAGGCUCUACGU 12

RESULT 49
US-08-192-942-7/c
; Sequence 7, Application US/08192942
; Patent No. 5989906
; GENERAL INFORMATION:
; APPLICANT: JAMES D. THOMPSON
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING P-GLYCOPROTEIN mdr-
; TITLE OF INVENTION: 1 GENE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/192,942
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/882,885
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 197/173
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600

```

TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-192-942-7
Query Match 30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 35;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 18 GGGAGTCCAG 27
||| |||||
Db 10 GGAAGTCCAG 1
||| |||||
RESULT 50
US-08-777-266A-85/c
Sequence 85, Application US/08777266A
Patent No. 6077833
GENERAL INFORMATION:
APPLICANT: Clarence Frank Bennett
APPLICANT: Timothy A. Vickers
TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the Expression of B7 Proteins
TITLE OF INVENTION: Methods for the Modulation of the Expression of B7 Proteins
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ
COUNTRY: USA
ZIP: 08002
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,266A
FILING DATE: December 31, 1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
US-08-777-266A-85
Query Match 30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 35;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 13 GTACAGGGAG 22
||| |||||
Db 10 GTACAGGGAG 1
||| |||||

RESULT 51
US-09-326-186B-85/c
Sequence 85, Application US/09326186B
Patent No. 6319906
GENERAL INFORMATION:
APPLICANT: Bennett, Clarence Frank
APPLICANT: Vickers, Timothy A.
TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
TITLE OF INVENTION: Modulation of the Expression of B7 Protein
FILE REFERENCE: ISPH-0376
CURRENT APPLICATION NUMBER: US/09/326,186B
CURRENT FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: 08/777,266
PRIOR FILING DATE: 1996-12-31
NUMBER OF SEQ ID NOS: 226
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 85
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-326-186B-85
Query Match 30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 35;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 13 GTACAGGGAG 22
||| |||||
Db 10 GTACAGGGAG 1
||| |||||
RESULT 52
US-09-769-482-14
Sequence 14, Application US/09769482
Patent No. 6566130
GENERAL INFORMATION:
APPLICANT: SRIVASTAVA, SHIV
APPLICANT: MOUL, JUDD W.
APPLICANT: XU, LINDA L.
TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
FILE REFERENCE: 04995.0057-00000
CURRENT APPLICATION NUMBER: US/09/769,482
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,772
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/179,045
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonucleotide
US-09-769-482-14
Query Match 30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 35;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 13 GTACAGGGAG 22
||| |||||
Db 1 GTGACGGGAG 10
||| |||||
RESULT 53
US-08-777-266A-86/c

; Sequence 86, Application US/08777266A
; Patent No. 6077833
; GENERAL INFORMATION:
; APPLICANT: Clarence Frank Bennett
; APPLICANT: Timothy A. Vickers
; TITLE OF INVENTION: Oligonucleotide Compositions and
; TITLE OF INVENTION: Methods for the Modulation of the Expression of B7 Proteins
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESS: Law Offices of Jane Massey Licata
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION NUMBER: US/08/777,266A
; FILING DATE: December 31, 1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0201
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-08-777-266A-86

Query Match 30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 GTACAGGGAG 22
DB 11 GTACGGGGAG 2

RESULT 54
US-09-326-186B-86/c
; Sequence 86, Application US/09326186B
; Patent No. 6319906
; GENERAL INFORMATION:
; APPLICANT: Bennett, Clarence Frank
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; TITLE OF INVENTION: Modulation of the Expression of B7 Protein
; FILE REFERENCE: ISPH-0376
; CURRENT APPLICATION NUMBER: US/09/326,186B
; CURRENT FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/777,266
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Synthetic
US-09-326-186B-86

Query Match 30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 GTACAGGGAG 22
DB 11 GTACGGGGAG 2

RESULT 55
US-09-249-155A-45/c
; Sequence 45, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-45

Query Match 30.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 TGTACAGGGA 21
DB 10 TGTACGGGGA 1

RESULT 56
US-08-623-891-39
; Sequence 39, Application US/08623891
; Patent No. 5795778
; GENERAL INFORMATION:
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HERPES SIMPLEX
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESS: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA: US/08/623,891
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/238,200
FILING DATE: 07/98/133
APPLICATION NUMBER: US/07/987,133
FILING DATE: 07/882,921
FILING DATE: May 14, 1992
APPLICATION NUMBER: 07/948,359
FILING DATE: September 18, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 200/209
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 12
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-623-891-39

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 70.0%; Pred. No. 51;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCTACGTGT 14
Db 1 CCGGACGUG 10

RESULT 57

US-08-494-301A-28/c
Sequence 28, Application US/08/494301A
Patent No. 5856461
GENERAL INFORMATION:
APPLICANT: Colote, Soudhir
APPLICANT: Piotzky, Eduardo
TITLE OF INVENTION: Oligonucleotides to inhibit the
TITLE OF INVENTION: Expression of Isoprenyl Protein Transferases
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lucas & Just
STREET: 205 E. 42nd Street
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10017
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
MEDIUM TYPE: 1.44 MB storage
COMPUTER: IBM 486 Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,301A
FILING DATE: 23-JUNE-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9413035.8
FILING DATE: 29-JUNE-1994
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleotide
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: Yes
US-08-494-301A-28

Query Match 30.0%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 9 ACCTGTACAG 18
Db 11 ACAGTACAG 2

RESULT 58

US-08-777-266A-87/c
Sequence 87, Application US/08/777266A
Patent No. 6077833
GENERAL INFORMATION:
APPLICANT: Clarence Frank Bennett
APPLICANT: Timothy A. Vickers
TITLE OF INVENTION: Oligonucleotide Compositions and
TITLE OF INVENTION: Methods for the Modulation of the Expression of B7 Proteins
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ
COUNTRY: USA
ZIP: 08002
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,266A
FILING DATE: December 31, 1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 12
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
US-08-777-266A-87

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 GTACAGGGAG 22
Db 12 GTACGGGGAG 3

RESULT 59

US-08-281-418-107/c
Sequence 107, Application US/09281418
Patent No. 6287769
GENERAL INFORMATION:
APPLICANT: Inoue, Takakazu
TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA
TITLE OF INVENTION: Method of Assaying Microorganisms, Method of Analyzing M
TITLE OF INVENTION: agment, Method of Assaying Microorganisms, Method of Assaying Contaminant
FILE REFERENCE: 9982-7
CURRENT APPLICATION NUMBER: US/09/281,418

; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: JP/1998/87651
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: JP/1999/69694
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 216
; SEQ ID NO 107
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-281-418-107

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CTACGTGTAC 16
Db 12 CTTCGTGTAC 3

RESULT 60
US-09-626-929-25
; Sequence 25, Application US/09626929
; Patent No. 6319714
; GENERAL INFORMATION:
; APPLICANT: CRAMERI, ANDREAS
; APPLICANT: STENMER, WILLEM P.C.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: BASS, STEVEN H.
; APPLICANT: WELCH, MARK
; APPLICANT: NESS, JON E.
; APPLICANT: GUSTAFSSON, CLAES
; APPLICANT: PATTEN, PHILIP A.
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION
; FILE REFERENCE: 02-029620US
; CURRENT APPLICATION NUMBER: US/09/626,929
; 2000-07-27
; CURRENT FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/408,392
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: 60/118,813
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/141,049
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(12)
US-09-626-929-25

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 GGGAGTCCAG 27
Db 2 GGGGTCCAG 11

RESULT 61
US-09-326-186B-87/c
; Sequence 87, Application US/09326186B
; Patent No. 6319906
; GENERAL INFORMATION:
; APPLICANT: Bennett, Clarence Frank

; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; FILE REFERENCE: ISPH-0376
; CURRENT APPLICATION NUMBER: US/09/326,186B
; CURRENT FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/777,266
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-326-186B-87

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 GTACGGGAG 22
Db 12 GTACGGGAG 3

RESULT 62
US-09-484-850-25
; Sequence 25, Application US/09484850
; Patent No. 6368861
; GENERAL INFORMATION:
; APPLICANT: CRAMERI, ANDREAS
; APPLICANT: STENMER, WILLEM P.C.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: BASS, STEVEN H.
; APPLICANT: WELCH, MARK
; APPLICANT: NESS, JON E.
; APPLICANT: GUSTAFSSON, CLAES
; APPLICANT: PATTEN, PHILIP A.
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION
; FILE REFERENCE: 02-029630US
; CURRENT APPLICATION NUMBER: US/09/484,850
; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/408,392
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: 60/118,813
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/141,049
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(12)
US-09-484-850-25

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 GGGAGTCCAG 27
Db 2 GGGGTCCAG 11

RESULT 63
US-09-408-392-25
; Sequence 25, Application US/09408392

```

; Patent No. 6376246
; GENERAL INFORMATION:
; APPLICANT: CRAMERI, ANDREAS
; APPLICANT: STEMMER, WILLEM P.C.
; APPLICANT: MINSHULL, JEREMY H.
; APPLICANT: BASS, STEVEN H.
; APPLICANT: WELCH, MARK
; APPLICANT: NESS, JON E.
; APPLICANT: GUSTAFSSON, CLAES
; APPLICANT: PATTEN, PHILLIP A.
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION
; FILE REFERENCE: 02-0296200S
; CURRENT APPLICATION NUMBER: US/09/408,392
; CURRENT FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: 60/118,813
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/141,049
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 25
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(12)
US-09-408-392-25

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 GGGAGTCCAG 27
DB 2 GGGGGTCCAG 11

RESULT 64
US-09-626-930-25
; Sequence 25, Application US/09626930
; Patent No. 6423542
; GENERAL INFORMATION:
; APPLICANT: CRAMERI, ANDREAS
; APPLICANT: STEMMER, WILLEM P.C.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: BASS, STEVEN H.
; APPLICANT: WELCH, MARK
; APPLICANT: NESS, JON E.
; APPLICANT: GUSTAFSSON, CLAES
; APPLICANT: PATTEN, PHILLIP A.
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION
; FILE REFERENCE: 02-0296200S
; CURRENT APPLICATION NUMBER: US/09/626,930
; CURRENT FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/408,392
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: 60/118,813
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/141,049
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 25
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(12)
US-09-626-930-25

Query Match 30.0%; Score 8.4; DB 1; Length 12;

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/340,861
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/987,133
; FILING DATE:
; APPLICATION NUMBER: 07/882,921
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: 07/948,359
; FILING DATE: September 18, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 200/209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-340-861-39

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 70.0%; Pred. No. 51;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCCTACGTGT 14
DB 1 CCCGACGUGU 10

RESULT 67
US-09-634-262-39
; Sequence 39, Application US/09634262
; Patent No. 6440719
; GENERAL INFORMATION:
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HERPES SIMPLEX
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/634,262
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/987,133
; FILING DATE:
; APPLICATION NUMBER: 07/882,921
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: 07/948,359
; FILING DATE: September 18, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 200/209

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-634-262-39

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 70.0%; Pred. No. 51;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCCTACGTGT 14
DB 1 CCCGACGUGU 10

RESULT 68
US-09-626-595-25
; Sequence 25, Application US/09626595
; Patent No. 6479652
; GENERAL INFORMATION:
; APPLICANT: CRAMERI, ANDREAS
; APPLICANT: STEMMER, WILLEM P.C.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: BASS, STEVEN H.
; APPLICANT: WELCH, MARK
; APPLICANT: NESS, JON E.
; APPLICANT: GUSTAFSSON, CLAES
; APPLICANT: PATTEN, PHILLIP A.
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION
; FILE REFERENCE: 02-029620US
; CURRENT APPLICATION NUMBER: US/09/626,595
; CURRENT FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/408,392
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: 60/118,813
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/141,049
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(12)
; US-09-626-595-25

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 GGGAGTCCAG 27
DB 2 GGGGTCAG 11

RESULT 69
US-09-694-863-25
; Sequence 25, Application US/09694863
; Patent No. 6521453
; GENERAL INFORMATION:
; APPLICANT: CRAMERI, ANDREAS
; APPLICANT: STEMMER, WILLEM P.C.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: BASS, STEVEN H.

```

APPLICANT: WELCH, MARK
APPLICANT: NESS, JON E.
APPLICANT: GUSTAFSSON, CLAES
APPLICANT: PATTEN, PHILIP A.
TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION
FILE REFERENCE: 02-029620US
CURRENT APPLICATION NUMBER: US/09/694,863
CURRENT FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 09/408,392
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: 60/141,049
PRIOR FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
LENGTH: 12
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(12)
US-09-694-863-25

Query Match 30.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 18 GGGAGTCCAG 27
Db 2 GGGGTCCAG 11

RESULT 70
US-08-702-665A-19/c
Sequence 19, Application US/08702665A
Patent No. 6274708
GENERAL INFORMATION:
APPLICANT: Hilton, Douglas J.
TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,665A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 10296
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 203 901 SANS UR
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-702-665A-19

Query Match 29.3%; Score 8.2; DB 1; Length 21;
Best Local Similarity 76.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 7 CTACGTGTACGG 19
Db 15 CTCACAGTACGG 3
RESULT 71
US-09-989-789-2098/c
Sequence 2098, Application US/09989789
Patent No. 6588746
GENERAL INFORMATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
FILE REFERENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2098
LENGTH: 9
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: example target
OTHER INFORMATION: DNA
US-09-989-789-2098

Query Match 28.6%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCCTACGT 12
Db 9 CCCTACGT 2

RESULT 72
US-09-989-789-2100/c
Sequence 2100, Application US/09989789
Patent No. 6588746
GENERAL INFORMATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
FILE REFERENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2100
LENGTH: 9
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: example target
OTHER INFORMATION: DNA
US-09-989-789-2100

Query Match 28.6%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCCTACGT 12
Db 9 CCCTACGT 2

RESULT 73
US-09-989-789-2195

; Sequence 2195, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2195
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2195

Query Match 28.6%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 AGGGAGTC 24
| | | | | | | | |
Db 2 AGGGAGTC 9

RESULT 74
US-09-989-789-2453/c
; Sequence 2453, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2453
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2453

Query Match 28.6%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCCCT 8
| | | | | | | | |
Db 9 CGGGCCCT 2

RESULT 75
US-09-989-789-2454/c
; Sequence 2454, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2454
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2454

Query Match 28.6%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCCCT 8
| | | | | | | | |
Db 9 CGGGCCCT 2

RESULT 76
US-08-170-095B-12
; Sequence 12, Application US/08170095B
; Patent No. 5563254
; GENERAL INFORMATION:
; APPLICANT: Hoffman, Stephen J.
; APPLICANT: Nagai, Kiyoshi
; TITLE OF INVENTION: Blood Substitutes
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Somatogen, Inc.
; STREET: 2545 Central Avenue
; CITY: Boulder
; STATE: Colorado
; ZIP: 80301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.0.1
; SOFTWARE: Microsoft Word 5.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/170,095B
; FILING DATE: December 20, 1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5563254ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: Hoffman 2A/CONT2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-541-3322
; TELEFAX: 303-444-3013
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown to applicant
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: ARTIFICIALLY GENERATED OLIGONUCLEOTIDE USED IN A CL
; HYPOTHETICAL: no
US-08-170-095B-12

Query Match 28.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCCCT 8
| | | | | | | | |
Db 3 CGGGCCCT 10

RESULT 77
US-08-396-866-12
; Sequence 12, Application US/08396866
; Patent No. 5661124

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,083
FILING DATE: 02-OCT-1991
APPLICATION NUMBER: FR 89 17467
FILING DATE: 29-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Bernhard D
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/318
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 693-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: oligonucleotide/primer of reverse
US-08-086-410-4

Query Match 28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCCCT 8
Db 5 CGGGCCCT 12

RESULT 81
US-07-939-501A-17
Sequence 17, Application US/07939501A
Patent No. 5446138
GENERAL INFORMATION:
APPLICANT: BLAISEAU, Pierre-Louis
APPLICANT: LEGOUX, Richard
APPLICANT: LEGUAY, Jean-Jacques
APPLICANT: SCHNEIDER, Michel
TITLE OF INVENTION: Recombinant DNA coding for a protein
TITLE OF INVENTION: having endochitinase activity
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: King Street Station, Suite 500, 1800 Diagonal
CITY: ALEXANDRIA
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/939,501A
FILING DATE: 19920908
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 11072
FILING DATE: 06-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Bernhard D
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/373
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300

TELEFAX: (703) 693-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-939-501A-17

Query Match 28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCCCT 8
Db 5 CGGGCCCT 12

RESULT 82
US-08-025-038-15/c
Sequence 15, Application US/08025038
Patent No. 5545526
GENERAL INFORMATION:
APPLICANT: BAXTER-LOWE, Lee-Ann
TITLE OF INVENTION: Method For HLA Typing
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 777 E. Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: USA
ZIP: 53202-5367
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/025,038
FILING DATE: 19930301
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/544,218
FILING DATE: 27-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Philip G.
REGISTRATION NUMBER: 30,478
REFERENCE/DOCKET NUMBER: 204 854
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414)289-3761
TELEFAX: (414)289-3791
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-08-025-038-15

Query Match 28.6%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCCCT 8
Db 9 CGGGCCCT 2

RESULT 83
US-08-152-955-4

```

; Sequence 4, Application US/08152955
; Patent No. 5474897
; GENERAL INFORMATION:
; APPLICANT: Weiss, Arthur
; TITLE OF INVENTION: Screening Assay for the Identification
; TITLE OF INVENTION: of Immunosuppressive Drugs
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/152,955
; CLASSIFICATION: 435
; APPLICATION DATA:
; PRIORITY APPLICATION NUMBER: US 07/898,639
; FILING DATE: 15-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/POCKET NUMBER: 2307U-356
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-152-955-4

Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred.No. 63;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 CAGGAGTCCA 26
Db 1 CAGAGATCCA 11

RESULT 84
US-09-249-155A-236
; Sequence 236, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 236
; LENGTH: 11
; TYPE: DNA

```

```

; ORGANISM: Mus musculus
US-09-249-155A-236
Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred.No. 63;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 18 GGGAGTCCAGG 28
Db 1 GGGGGCCAGG 11

RESULT 85
US-09-249-155A-272/C
; Sequence 272, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 272
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-272

Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred.No. 63;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CGTGTACAGG 20
Db 11 CTGTAGAGG 1

RESULT 86
PCT-US93-05668-4
; Sequence 4, Application PC/TUS9305668
; GENERAL INFORMATION:
; APPLICANT: Weiss, Arthur
; APPLICANT: Fraser, James
; TITLE OF INVENTION: Screening Assay for the Identification
; TITLE OF INVENTION: of Immunosuppressive Drugs
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fisher & Amzel
; STREET: 1320 Harbor Bay Parkway, Suite 225
; CITY: Alameda
; STATE: California
; COUNTRY: USA
; ZIP: 94501
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05668
; FILING DATE: 19930611
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,639

```


FILING DATE: 15-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fisher, Stanley P.
REGISTRATION NUMBER: 24,344
REFERENCE/DOCKET NUMBER: 81-143-1PCT
TELEPHONE: 510-748-6868
TELEFAX: 510-748-6688
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US93-05668-4

Query Match 27.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 63;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 CAGGAGGATCCA 26
||| ||| ||| |||
Db 1 CAGAGATTCCA 11

RESULT 87
US-08-035-928-19/c
Sequence 19, Application US/08035928
Patent No. 5538844
GENERAL INFORMATION:
APPLICANT: Duyao, Mabel P.
APPLICANT: MacDonald, Marcy E.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: A No. 5538844el Transport Protein Gene from
the Huntington's Disease Region
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Avenue N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/035,928
FILING DATE: 19930323
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 466-0800
TELEFAX: (202) 833-8716
TELEX:
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: both
TOPOLOGY: linear

US-08-035-928-19
Query Match 27.9%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 74;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCCTACGTTGA 15
||||| |||
Db 12 CCCTACTGAA 2

RESULT 88
US-08-435-350-107/c
Sequence 107, Application US/08435350
Patent No. 5599704
GENERAL INFORMATION:
APPLICANT: James D. Thompson
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: METHOD AND REAGENT FOR
TREATMENT OF BREAST CANCER
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,350
FILING DATE: 05-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/936,531
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 197/245
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 12
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-435-350-107
Query Match 27.9%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 74;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCCTACGTTGT 14
||| ||| ||| |||
Db 12 GCCGTAGTTGT 2

RESULT 89
US-08-494-301A-25/c
Sequence 25, Application US/08494301A
Patent No. 5856461
GENERAL INFORMATION:
APPLICANT: Colote, Soudhir
APPLICANT: Pilote, Eduardo
TITLE OF INVENTION: Oligonucleotides to Inhibit the
Expression of Isoprenyl Protein Transferases
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lucas & Just
STREET: 205 E. 42nd Street
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10017

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch,
MEDIUM TYPE: 1.44 MB storage
COMPUTER: IBM 486 Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION NUMBER: US/08/494,301A
APPLICATION NUMBER: US/08/494,301A
FILING DATE: 23-JUNE-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9413035.8
FILING DATE: 29-JUNE-1994
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleotide
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: Yes
US-08-494-301A-25

Query Match 27.9%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 74;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 GTACAGGAGT 23
DB 11 GTCCAGAGT 1

RESULT 90

US-09-281-418-25/c
Sequence 25, Application US/09281418
Patent No. 6287769
GENERAL INFORMATION:
APPLICANT: Inoue, Takakazu
TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA F
TITLE OF INVENTION: agent, Method of Assaying Microorganisms, Method of Analyzing Mi
TITLE OF INVENTION: nisms and Method of Assaying Contaminant
FILE REFERENCE: 9982-7
CURRENT APPLICATION NUMBER: US/09/281.418
CURRENT FILING DATE: 1999-03-30
EARLIER APPLICATION NUMBER: JP/1998/87651
EARLIER FILING DATE: 1998-03-31
EARLIER APPLICATION NUMBER: JP/1999/69694
EARLIER FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 216
SEQ ID NO 25
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-281-418-25

Query Match 27.9%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 74;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CTACGTGTACA 17
DB 11 CTTCGTGTAGA 1

RESULT 91

US-09-528-404-9
Sequence 9, Application US/09528404
Patent No. 6440723
GENERAL INFORMATION:
APPLICANT: Roderic M.K. Dale
TITLE OF INVENTION: ARRAYS WITH MODIFIED OLIGONUCLEOTIDE AND
TITLE OF INVENTION: POLYNUCLEOTIDE COMPOSITIONS
FILE REFERENCE: OLIG-002CIP3

CURRENT APPLICATION NUMBER: US/09/528,404
CURRENT FILING DATE: 2000-03-17
EARLIER APPLICATION NUMBER: 09/223,498
EARLIER FILING DATE: 1998-12-30
EARLIER APPLICATION NUMBER: 09/408,088
EARLIER FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 12
TYPE: RNA
ORGANISM: rat
US-09-528-404-9

Query Match 27.9%; Score 7.8; DB 1; Length 12;
Best Local Similarity 72.7%; Pred. No. 74;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 15 ACAGGGAGTCC 25
DB 1 AUAAGGGAUCC 11

RESULT 92

US-08-717-526-61/c
Sequence 61, Application US/08717526
Patent No. 5786147
GENERAL INFORMATION:
APPLICANT: MABILAT, CLAUDE
APPLICANT: RAOULT, DIDIER
TITLE OF INVENTION: DETECTION OF ENTEROBACTERIA
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & HERRIDGE
STREET: 700 SOUTH WASHINGTON STREET
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,526
FILING DATE: 17-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 38732
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-717-526-61

Query Match 26.4%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGGAGT 23
DB 9 ACAGAGAT 1

```
RESULT 93
US-09-153-242-30
; Sequence 30, Application US/09153242
; Patent No. 6482592
; GENERAL INFORMATION:
; APPLICANT: Lundberg, Joakim
; APPLICANT: Uhlen, Mathias
; TITLE OF INVENTION: MODULAR PROBES II
; FILE REFERENCE: 1181-242
; CURRENT APPLICATION NUMBER: US/09/153,242
; CURRENT FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: PCT/GB97/02629
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide H1-9
US-09-153-242-30

Query Match      26.4%; Score 7.4; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.1e+02;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GGGCCCTAC 10
Db      1 GGGCCCTCC 9

RESULT 94
US-07-651-710A-33/c
; Sequence 33, Application US/07651710A
; Patent No. 5362864
; GENERAL INFORMATION:
; APPLICANT: Chua, Nam-Hai
; TITLE OF INVENTION: Trans-Activating Factor-1
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/651,710A
; FILING DATE: 19910206
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 3288-014
; TELEPHONE: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: TAF-1 binding motif
US-07-651-710A-33

Query Match      26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 CTACGTGTA 15
Db      9 CCACGTGTA 1

RESULT 95
US-07-651-710A-38/c
; Sequence 38, Application US/07651710A
; Patent No. 5362864
; GENERAL INFORMATION:
; APPLICANT: Chua, Nam-Hai
; TITLE OF INVENTION: Trans-Activating Factor-1
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/651,710A
; FILING DATE: 19910206
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 3288-014
; TELEPHONE: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: TAF-1 binding motif
US-07-651-710A-38

Query Match      26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 CTACGTGTA 15
Db      9 CCACGTGTA 1

RESULT 96
US-08-074-879-3
; Sequence 3, Application US/08074879
; Patent No. 5656423
; GENERAL INFORMATION:
; APPLICANT: Orth, Gerard
; APPLICANT: Volpers, Christoph
; APPLICANT: Streek, Rolf
; TITLE OF INVENTION: DNA Sequences Derived from the Genome of
; TITLE OF INVENTION: the Papillomavirus HPV39, Their Use in In Vitro Diagnosis
; TITLE OF INVENTION: and for the Production of an Immunogenic Composition
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/074,879
FILING DATE: 16-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/1136
FILING DATE: 09-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 02356.0066-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-074-879-3

Query Match 26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGGAGT 23
| | | | |
DB 1 AAAGGGAGT 9

RESULT 97
US-08-468-057A-3
Sequence 3, Application US/08468057A
Patent No. 568535
GENERAL INFORMATION:
APPLICANT: Orth, Gerard
APPLICANT: Volpers, Christoph
APPLICANT: Streek, Rolf
TITLE OF INVENTION: DNA Sequences Derived from the Genome of
TITLE OF INVENTION: the Papillomavirus HPV39, Their Use in In Vitro Diagnosis
TITLE OF INVENTION: and for the Production of an Immunogenic Composition
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,057A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/074,879
FILING DATE: 16-JUN-1993
APPLICATION NUMBER: WO 92/1136
FILING DATE: 09-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 02356.0066-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-468-057A-3

Query Match 26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGGAGT 23
| | | | |
DB 1 AAAGGGAGT 9

RESULT 98
US-08-378-986-6
Sequence 6, Application US/08378986
Patent No. 5723751
GENERAL INFORMATION:
APPLICANT: Chua, Nam-Hai
TITLE OF INVENTION: Expression Motifs That Confer
TITLE OF INVENTION: Tissue- and Developmental-Specific Expression in Plants
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,986
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/982,792
FILING DATE: 30-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 3288-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: Opaque 2 binding site

US-08-378-986-6

Query Match 26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CTACGTGTA 15
| | | | | | | |
Db 2 CTACGTGGA 10

RESULT 99

US-08-388-353-495/c
; Sequence 495, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 495:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-495

Query Match 26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGGAGT 23
| | | | | | | |
Db 10 ACAGGGGTG 2

RESULT 100

US-08-388-353-496/c
; Sequence 496, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.

; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 496:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-496

Query Match 26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGGAGT 23
| | | | | | | |
Db 9 ACAGGGGTG 1

RESULT 101

US-08-388-353-657/c
; Sequence 657, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995

```
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 657:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-657

Query Match 26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 GTACAGGGA 21
DB 10 GTACAGGCA 2

RESULT 102
US-08-388-353-658/c
; Sequence 658, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 658:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-658

Query Match 26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 TGTACGGG 20
DB 2 TGTACTGG 10

RESULT 104
US-08-388-353-662
; Sequence 662, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
```

```

; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 662:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-662

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```

Query Match 26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 TGTACAGG 20
DB 1 TGTACTGG 9

```

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RESULT 105
US-08-488-551B-495/C
; Sequence 495, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994

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; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 495:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-495

Query Match 26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 ACAGGGAGT 23
DB 10 ACAGGGTGT 2

```

```

RESULT 106
US-08-488-551B-496/C
; Sequence 496, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 496:

```

SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-496

Query Match 26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 15 ACAGGGAGT 23
Db 9 ACAGGGTGT 1

RESULT 107

US-08-488-551B-657/c
; Sequence 657, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGILIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 657:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-657

Query Match 26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 GTACAGGGA 21

Db 10 GTACAGGCA 2

RESULT 108

US-08-488-551B-658/c
; Sequence 658, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGILIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 658:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-658

Query Match 26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 GTACAGGGA 21

Db 9 GTACAGGCA 1

RESULT 109

US-08-488-551B-661
; Sequence 661, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1

NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSER: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 96062
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 661:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-661

Query Match 26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 TGTACAGGG 20
|||||
Db 2 TGTACTGGG 10

RESULT 110
US-08-488-551B-662
Sequence 662, Application US/08488551B
Patent No. 6015661
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 96062
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 662:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-662

Query Match 26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 TGTACAGGG 20
|||||
Db 1 TGTACTGGG 9

RESULT 111
US-08-488-551B-813/c
Sequence 813, Application US/08488551B
Patent No. 6015661
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM3021/95

; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 813:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-813

Query Match 26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 15 ACAGGGAGT 23
Db 10 ACAGGGGT 2

RESULT 112
US-08-488-551B-814/c
; Sequence 814, Application US/08488551B
; Patent No. 6015861
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 814:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: DNA
US-08-488-551B-814

Query Match 26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 15 ACAGGGAGT 23
Db 9 ACAGGGGT 1

RESULT 113
US-08-522-384-34/c
; Sequence 34, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-34

Query Match 26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 TGTACAGGG 20
Db 10 TGTACATGG 2

RESULT 114
US-09-425-798-12/c
; Sequence 12, Application US/09425798A
; Patent No. 6423493
; GENERAL INFORMATION:
; APPLICANT: Gorenstein Dr., David G.
; APPLICANT: King Dr., David J.
; APPLICANT: Ventura, Daniel A.
; APPLICANT: Brasier Dr., Allan R.
; TITLE OF INVENTION: Combinatorial Selection of Phosphothionate
; TITLE OF INVENTION: Oligonucleotide Aptamers
; FILE REFERENCE: 122144-1005
; CURRENT APPLICATION NUMBER: US/09/425,798A
; CURRENT FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 60/105,600
; FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: aptamer
US-09-425-798-12

Query Match 26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY      10 CCGTGTACAG 18
      | | | | | | |
Db      10 CATGTACAG 2

RESULT 115
US-09-154-750A-17/c
; Sequence 17, Application US/09154750A
; Patent No. 6432640
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/059,153
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079817
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-154-750A-17

Query Match      26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      16 CAGGGAGTC 24
      | | | | | | |
Db      10 CAGGGAGTC 2

RESULT 116
US-09-154-750A-37
; Sequence 37, Application US/09154750A
; Patent No. 6432640
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/059,153
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079817
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-154-750A-37

Query Match      26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      8 TACGTGTAC 16
      | | | | | |
Db      2 TAAGGTAC 10

RESULT 117
US-09-462-561B-26/c

; Sequence 26, Application US/09462561B
; Patent No. 6455252
; GENERAL INFORMATION:
; APPLICANT: Wade, Nicholas M.
; APPLICANT: Harrison, Bruce T.
; APPLICANT: King, Brian W.
; APPLICANT: Reed, Kenneth C.
; APPLICANT: Murphy, Kathleen M.
; TITLE OF INVENTION: DETERMINATION OF GENETIC SEX IN EQUINE SPECIES BY
; FILE REFERENCE: ANALYSIS OF Y-CHROMOSOMAL DNA SEQUENCES
; CURRENT APPLICATION NUMBER: US/09/462,561B
; CURRENT FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: P07802
; PRIOR FILING DATE: 1997-07-09
; PRIOR APPLICATION NUMBER: PCT/AU98/00533
; PRIOR FILING DATE: 1998-07-08
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Equus caballus
US-09-462-561B-26

Query Match      26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      5 CCGTACGTG 13
      | | | | |
Db      10 CCGTACGTG 2

RESULT 118
US-09-301-721A-27/c
; Sequence 27, Application US/09301721A
; Patent No. 6506561
; GENERAL INFORMATION:
; APPLICANT: CHEVAL, Lydie
; APPLICANT: ELALOUF, Jean-Marc
; APPLICANT: VIRLON, Berangere
; TITLE OF INVENTION: MICROASSAY FOR SERIAL ANALYSIS OF GENE EXPRESSION AND
; FILE REFERENCE: 0846-0499-0X
; CURRENT APPLICATION NUMBER: US/09/301,721A
; CURRENT FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: BFO 99400189.9
; PRIOR FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic DNA
US-09-301-721A-27

Query Match      26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      13 GTACAGGGA 21
      | | | | |
Db      10 GCACAGGGA 2

RESULT 119
US-09-508-753B-160/c
; Sequence 160, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
```

; APPLICANT: Akira SHIMAMOTO
 ; APPLICANT: Yasuhiro FURUICHI
 ; APPLICANT: YUKO SHIBATA
 ; APPLICANT: HIROKO FUNAKI
 ; APPLICANT: Eiji OHARA
 ; APPLICANT: Masanori WATAHAKI
 ; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
 ; FILE REFERENCE: 00162/HG
 ; CURRENT APPLICATION NUMBER: US/09/508,753B
 ; CURRENT FILING DATE: 2000-06-16
 ; PRIOR APPLICATION NUMBER: JP 9/270324
 ; PRIOR FILING DATE: 1997-09-18
 ; NUMBER OF SEQ ID NOS: 472
 ; SEQ ID NO 160
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Primer
 US-09-508-753B-160

Query Match 26.4%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 66;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 19 GGAGTCCAG 27
 Db 10 GGAGTCCAG 2

RESULT 120

US-09-769-482-18/c
 ; Sequence 18, Application US/09769482
 ; Patent No. 6566130

; GENERAL INFORMATION:
 ; APPLICANT: SRIVASTAVA, SHIV
 ; APPLICANT: MOUL, JUDD W.
 ; APPLICANT: XU, LINDA L.
 ; APPLICANT: SEGAWA, TAKEHIKO
 ; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
 ; FILE REFERENCE: FOYNUCLEOTIDE ARRAY
 ; CURRENT APPLICATION NUMBER: US/09/769,482
 ; CURRENT FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: 60/178,772
 ; PRIOR FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: 60/179,045
 ; PRIOR FILING DATE: 2000-01-31
 ; NUMBER OF SEQ ID NOS: 67
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 18
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: oligonucleotide

Query Match 26.4%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 66;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GTGTACAG 19
 Db 9 GGGTACAG 1

RESULT 121

US-09-504-132-10/c
 ; Sequence 10, Application US/09504132
 ; Patent No. 6582899
 ; GENERAL INFORMATION:

; APPLICANT: Kamb, Carl Alexander
 ; APPLICANT: Caponigro, Giordano Michael
 ; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGENTS THAT CAUSE A LETHAL
 ; FILE REFERENCE: PHENOTYPE, AND AGENTS THEREOF
 ; FILE REFERENCE: 29345/36169
 ; CURRENT APPLICATION NUMBER: US/09/504,132
 ; CURRENT FILING DATE: 2000-02-15
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic -
 ; OTHER INFORMATION: Aptamer 4
 US-09-504-132-10

Query Match 26.4%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 66;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 20 GAGTCCAGG 28
 Db 10 GAGTCCAGG 2

RESULT 122

US-09-989-789-1630
 ; Sequence 1630, Application US/09989789
 ; Patent No. 6588746

; GENERAL INFORMATION:
 ; APPLICANT: LIU, Qiang
 ; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
 ; FILE REFERENCE: TRIPLETS BY ZINC FINGERS
 ; FILE REFERENCE: 8325-0011.20 / S11-US2
 ; CURRENT APPLICATION NUMBER: US/09/989,789
 ; CURRENT FILING DATE: 2002-03-25
 ; NUMBER OF SEQ ID NOS: 4085
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1630
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: example target
 ; OTHER INFORMATION: DNA
 US-09-989-789-1630

Query Match 26.4%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 66;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 17 AGGAGTCC 25
 Db 2 AGGAGTCC 10

RESULT 123

US-09-989-789-1631
 ; Sequence 1631, Application US/09989789
 ; Patent No. 6588746

; GENERAL INFORMATION:
 ; APPLICANT: LIU, Qiang
 ; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
 ; FILE REFERENCE: TRIPLETS BY ZINC FINGERS
 ; FILE REFERENCE: 8325-0011.20 / S11-US2
 ; CURRENT APPLICATION NUMBER: US/09/989,789
 ; CURRENT FILING DATE: 2002-03-25
 ; NUMBER OF SEQ ID NOS: 4085
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1631
 ; LENGTH: 10

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1631

Query Match 26.4%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 17 AGGAGTTC 25
||| |||
Db 2 AGGAGTTC 10

RESULT 124
US-07-951-715A-55/C
; Sequence 55, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Wright, Martha S.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
TELEPHONE: (919)541-8615
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "primer for third quarter -
; DESCRIPTION: first half"
; HYPOTHETICAL: NO
US-07-951-715A-55

Query Match 26.4%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 TACAGGAG 22
||| |||
Db 11 TACAGGAG 3

RESULT 125
US-08-459-448A-55/C
; Sequence 55, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5859336artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; STREET: Rd., POB 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer for third quarter -
DESCRIPTION: first half"
HYPOTHETICAL: NO
US-08-459-448A-55

Query Match 26.4%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 TACAGGGGAG 22
Db 11 TACAGGGGG 3

RESULT 126

US-08-459-595A-55/c
Sequence 55, Application US/08459595A
Patent No. 6018104

GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6018104artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
City: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,595A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer for third quarter -
DESCRIPTION: first half"
HYPOTHETICAL: NO
US-08-459-595A-55

Query Match 26.4%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 TACAGGGGAG 22
Db 11 TACAGGGGG 3

RESULT 127

US-08-459-504B-55/c
Sequence 55, Application US/08459504B
Patent No. 6075185

GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6075185artis Corporation
STREET: 3054 Cornwallis Road
City: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689

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; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer for third quarter -
; DESCRIPTION: first half"
; HYPOTHETICAL: NO
; US-08-459-504B-55

Query Match          26.4%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      14 TACAGGGGAG 22
Db      11 TACAGGGGG 3

RESULT 128
US-08-459-444-55/c
; Sequence 55, Application US/08459444A
; Patent No. 6121014
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
; TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
; NUCLEIC ACID CODING SEQUENCE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,444A
; FILING DATE: 02-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer for third quarter -
; DESCRIPTION: first half"
; HYPOTHETICAL: NO
; US-08-459-504B-55

Query Match          26.4%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      14 TACAGGGGAG 22
Db      11 TACAGGGGG 3

RESULT 129
US-09-547-422-55/c
; Sequence 55, Application US/09547422
; Patent No. 6320100
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/547,422
; FILING DATE: 11-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/459,595
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-18805H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer for third quarter -
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 55:
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US-09-547-422-55

Query Match 26.4%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 80;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 14 TACAGGGAG 22
 |||||
 Db 11 TACAGGGG 3

RESULT 130

US-09-153-242-29
 ; Sequence 29, Application US/09153242
 ; Patent No. 6482592
 ; GENERAL INFORMATION:
 ; APPLICANT: Lundberg, Joakim
 ; APPLICANT: Uhlen, Mathias
 ; TITLE OF INVENTION: MODULAR PROBES II
 ; FILE REFERENCE: 1181-242
 ; CURRENT APPLICATION NUMBER: US/09/153,242
 ; CURRENT FILING DATE: 1998-09-15
 ; PRIOR APPLICATION NUMBER: PCT/GB97/02629
 ; PRIOR FILING DATE: 1997-09-26
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 29
 ; LENGTH: 11
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: oligonucleotide HI-11
 US-09-153-242-29

Query Match 26.4%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 80;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGCCCTAC 10
 |||||
 Db 3 GGGCCCTCC 11

RESULT 131

US-09-249-155A-61/c
 ; Sequence 61, Application US/09249155A
 ; Patent No. 6538173
 ; GENERAL INFORMATION:
 ; APPLICANT: Heber-Katz, Ellen
 ; TITLE OF INVENTION: Compositions and Methods for Wound
 ; FILE REFERENCE: 00486.78503
 ; CURRENT APPLICATION NUMBER: US/09/249,155A
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074,737
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: US 60/097,937
 ; PRIOR FILING DATE: 1998-08-26
 ; PRIOR APPLICATION NUMBER: US 60/102,051
 ; PRIOR FILING DATE: 1998-09-28
 ; NUMBER OF SEQ ID NOS: 346
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 61
 ; LENGTH: 11
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-09-249-155A-61

Query Match 26.4%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 80;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GTGTACAGG 19
 |||||
 Db 11 GTGTCCAGG 3

RESULT 132

US-09-249-155A-162
 ; Sequence 162, Application US/09249155A
 ; Patent No. 6538173
 ; GENERAL INFORMATION:
 ; APPLICANT: Heber-Katz, Ellen
 ; TITLE OF INVENTION: Compositions and Methods for Wound
 ; FILE REFERENCE: 00486.78503
 ; CURRENT APPLICATION NUMBER: US/09/249,155A
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074,737
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: US 60/097,937
 ; PRIOR FILING DATE: 1998-08-26
 ; PRIOR APPLICATION NUMBER: US 60/102,051
 ; PRIOR FILING DATE: 1998-09-28
 ; NUMBER OF SEQ ID NOS: 346
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 162
 ; LENGTH: 11
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-09-249-155A-162

Query Match 26.4%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 80;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 GTACAGGGA 21
 |||||
 Db 3 GTCCAGGGA 11

RESULT 133

US-09-249-155A-203/c
 ; Sequence 203, Application US/09249155A
 ; Patent No. 6538173
 ; GENERAL INFORMATION:
 ; APPLICANT: Heber-Katz, Ellen
 ; TITLE OF INVENTION: Compositions and Methods for Wound
 ; FILE REFERENCE: 00486.78503
 ; CURRENT APPLICATION NUMBER: US/09/249,155A
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074,737
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: US 60/097,937
 ; PRIOR FILING DATE: 1998-08-26
 ; PRIOR APPLICATION NUMBER: US 60/102,051
 ; PRIOR FILING DATE: 1998-09-28
 ; NUMBER OF SEQ ID NOS: 346
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 203
 ; LENGTH: 11
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-09-249-155A-203

Query Match 26.4%; Score 7.4; DB 1; Length 11;
 Best Local Similarity 88.9%; Pred. No. 80;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GTGTACAGG 19
 |||||
 Db 11 GTGTCCAGG 3


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;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA oligonucleotide"
US-08-633-792A-6

Query Match      26.4%; Score 7.4; DB 1; Length 18;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      11 GTGTACAGGGAGTCCAG 27
DB      2 GTGACTCGCTGTACAG 18

RESULT 136
US-09-075-717A-6
; Sequence 6, Application US/09075717A
; Patent No. 6174869
; GENERAL INFORMATION:
; APPLICANT: Barrett, Graham L
; TITLE OF INVENTION: A METHOD FOR ENHANCING NEURONE SURVIVAL
; TITLE OF INVENTION: AND AGENTS USEFUL FOR SAME
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/075,717A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/633,792
; FILING DATE: 01-JUL-1996
; APPLICATION NUMBER: AU PM/1870
; FILING DATE: 18-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516)742-4343
; TELEFAX: (516)742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; APPLICATION TYPE: other nucleic acid
; MOLECULE TYPE: /desc = "DNA oligonucleotide"
US-09-075-717A-6

Query Match      26.4%; Score 7.4; DB 1; Length 18;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      11 GTGTACAGGGAGTCCAG 27
DB      2 GTGACTCGCTGTACAG 18

;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA oligonucleotide"
US-08-633-792A-6

Query Match      26.4%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGGAGTC 24
DB      11 CAGGGAGAC 3

RESULT 135
US-08-633-792A-6
; Sequence 6, Application US/08633792A
; Patent No. 5837694
; GENERAL INFORMATION:
; APPLICANT: Barrett, Graham L
; TITLE OF INVENTION: A METHOD FOR ENHANCING NEURONE SURVIVAL
; TITLE OF INVENTION: AND AGENTS USEFUL FOR SAME
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,792A
; FILING DATE: 01-JUL-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PM/1870
; FILING DATE: 18-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516)742-4343
; TELEFAX: (516)742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; APPLICATION TYPE: other nucleic acid
; MOLECULE TYPE: /desc = "DNA oligonucleotide"
US-08-633-792A-6

Query Match      26.4%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGGAGTC 24
DB      11 CAGGGAGAC 3

RESULT 134
US-09-249-155A-231/G
; Sequence 231, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; HEALING
; FILE REFERENCE: 00486, 78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-231

Query Match      26.4%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 80;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 CAGGGAGTC 24
DB      11 CAGGGAGAC 3

RESULT 135
US-08-633-792A-6
; Sequence 6, Application US/08633792A
; Patent No. 5837694
; GENERAL INFORMATION:
; APPLICANT: Barrett, Graham L
; TITLE OF INVENTION: A METHOD FOR ENHANCING NEURONE SURVIVAL
; TITLE OF INVENTION: AND AGENTS USEFUL FOR SAME
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,792A
; FILING DATE: 01-JUL-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PM/1870
; FILING DATE: 18-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516)742-4343
; TELEFAX: (516)742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; APPLICATION TYPE: other nucleic acid
; MOLECULE TYPE: /desc = "DNA oligonucleotide"
US-08-633-792A-6

Query Match      26.4%; Score 7.4; DB 1; Length 18;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      11 GTGTACAGGGAGTCCAG 27
DB      2 GTGACTCGCTGTACAG 18

;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA oligonucleotide"
US-08-633-792A-6

Query Match      26.4%; Score 7.4; DB 1; Length 18;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      11 GTGTACAGGGAGTCCAG 27
DB      2 GTGACTCGCTGTACAG 18
```

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RESULT 137
US-08-327-525A-35
; Sequence 35, Application US/08327525A
; Patent No. 5795716
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark S.
; APPLICANT: Wang, Chunwei
; APPLICANT: Jevons, Luis C.
; APPLICANT: Bernhart, Derek H.
; APPLICANT: Lipshutz, Robert J.
; TITLE OF INVENTION: Computer-Aided Visualization and
; TITLE OF INVENTION: Analysis System for Sequence Evaluation
; Patent No. 5795716
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,525A
; FILING DATE: October 21, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5795716viel, Vernon A.
; REGISTRATION NUMBER: 32,483
; REFERENCE/DOCKET NUMBER: 16528X-82
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; US-08-327-525A-35
;
Query Match 25.7%; Score 7.2; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 15 ACAGGGAG 22
Db 1 ACAGGRR 8

RESULT 138
US-08-531-137B-35
; Sequence 35, Application US/08531137B
; Patent No. 5974164
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark S.
; TITLE OF INVENTION: Computer-Aided Visualization and
; TITLE OF INVENTION: Analysis System for Sequence Evaluation
; Patent No. 5974164
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ritter, Van Pelt & Yi LLP
; STREET: 4906 El Camino Real, Suite 205
; CITY: Los Altos
; STATE: California
; COUNTRY: USA
; ZIP: 94022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/158,765
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 08/531,137
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ritter, Michael J.
; REGISTRATION NUMBER: 36,653
; REFERENCE/DOCKET NUMBER: AFFY006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-903-3500
; TELEFAX: 650-903-3501
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; MOLECULE TYPE: DNA (oligonucleotide)
; US-08-531-137B-35

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/531,137B
; FILING DATE: October 16, 1995
; CLASSIFICATION: 382
; ATTORNEY/AGENT INFORMATION:
; NAME: Ritter, Michael J.
; REGISTRATION NUMBER: 36,653
; REFERENCE/DOCKET NUMBER: AFFY006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-903-3500
; TELEFAX: 650-903-3501
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; US-08-531-137B-35
;
Query Match 25.7%; Score 7.2; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 15 ACAGGGAG 22
Db 1 ACAGGRR 8

RESULT 139
US-09-158-765-35
; Sequence 35, Application US/09158765
; Patent No. 6242180
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark S.
; TITLE OF INVENTION: Computer-Aided Visualization and
; TITLE OF INVENTION: Analysis System for Sequence Evaluation
; Patent No. 6242180
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ritter, Van Pelt & Yi LLP
; STREET: 4906 El Camino Real, Suite 205
; CITY: Los Altos
; STATE: California
; COUNTRY: USA
; ZIP: 94022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/158,765
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 08/531,137
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ritter, Michael J.
; REGISTRATION NUMBER: 36,653
; REFERENCE/DOCKET NUMBER: AFFY006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-903-3500
; TELEFAX: 650-903-3501
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; MOLECULE TYPE: DNA (oligonucleotide)
; US-08-531-137B-35

```

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
US-09-158-765-35

Query Match      25.7%; Score 7.2; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      15 ACAGGGAG 22
DB      1 ACAGGRR  8

RESULT 140
US-09-796-071-35
; Sequence 35, Application US/09796071
; Patent No. 6607887
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark S.
; TITLE OF INVENTION: Computer-Aided Visualization and
; Analysis System for Sequence Evaluation
; Patent No. 6607887
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ritter, Van Pelt & Yi LLP
; STREET: 4906 El Camino Real, Suite 205
; CITY: Los Altos
; STATE: California
; COUNTRY: USA
; ZIP: 94022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/796,071
; FILING DATE: 27-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/531,137
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ritter, Michael J.
; REGISTRATION NUMBER: 36,653
; REFERENCE/DOCKET NUMBER: APTYP006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-903-3500
; TELEFAX: 650-903-3501
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-796-071-35

Query Match      25.7%; Score 7.2; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      15 ACAGGGAG 22
DB      1 ACAGGRR  8

RESULT 141
US-09-281-418-107
; Sequence 107, Application US/09281418
; Patent No. 6287769
; GENERAL INFORMATION:
; APPLICANT: Inoue, Takakazu
; TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA
; Fragment, Method of Assaying Microorganisms, Method of Analyzing
; Microorganisms, Method of Assaying Contaminant
; FILE REFERENCE: 9982-7
; CURRENT APPLICATION NUMBER: US/09/281,418
; CURRENT FILING DATE: 1999-03-30
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: JP/1999/69694
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 216
; SEQ ID NO 107
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-281-418-107

Query Match      25.7%; Score 7.2; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      11 GTGTACAGGGAG 22
DB      1 GAGTACAGGAG 12

RESULT 142
US-09-281-418-25
; Sequence 25, Application US/09281418
; Patent No. 6287769
; GENERAL INFORMATION:
; APPLICANT: Inoue, Takakazu
; TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA
; Fragment, Method of Assaying Microorganisms, Method of Analyzing
; Microorganisms, Method of Assaying Contaminant
; FILE REFERENCE: 9982-7
; CURRENT APPLICATION NUMBER: US/09/281,418
; CURRENT FILING DATE: 1999-03-30
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: JP/1999/69694
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 216
; SEQ ID NO 25
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-281-418-25

Query Match      25.7%; Score 7.2; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      12 TGTACAGGGAGT 23
DB      1 TCTACAGGAGT 12

RESULT 143
US-08-182-968A-297/c
; Sequence 297, Application US/08182968A
; Patent No. 5610054
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
```

NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,968A
FILING DATE: 13-JANUARY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/882,888
FILING DATE: 14-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 205/277
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 297:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-182-968A-297

Query Match 25.7%; Score 7.2; DB 1; Length 15;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 15 ACAGGGAGTCCA 26
DB 13 ACCTGGACTCCA 2

RESULT 144
US-08-774-306A-297/c
Sequence 297, Application US/08774306A
Patent No. 5869253
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING HEPATITIS C
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 07/882,888
FILING DATE: April 21, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/774,306
FILING DATE: December 26, 1996
APPLICATION NUMBER: 08/182,968
FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/882,888
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 234/083
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 297:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/182,968
FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/882,888
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/227
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 297:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-774-306A-297

Query Match 25.7%; Score 7.2; DB 1; Length 15;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 15 ACAGGGAGTCCA 26
DB 13 ACCTGGACTCCA 2

RESULT 145
US-09-064-156A-297/c
Sequence 297, Application US/09064156A
Patent No. 6132966
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING HEPATITIS C
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 498
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,156A
FILING DATE: April 21, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/774,306
FILING DATE: December 26, 1996
APPLICATION NUMBER: 08/182,968
FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/882,888
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 234/083
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 297:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-064-156A-297

Query Match 25.0%; Score 7.2; DB 1; Length 15;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 15 ACAGGAGTGCTCA 26
Db 13 ACCTGGAGTCTCA 2

RESULT 146
US-08-859-954-179
; Sequence 179, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 179:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-859-954-179

Query Match 25.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 GAGTCTCA 26
Db 1 GAGTCTCA 7

RESULT 147
US-08-859-954-289/c
; Sequence 289, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 289:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-859-954-289

Query Match 25.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 AGTCCAG 27
Db 7 AGTCCAG 1

RESULT 148
US-08-859-954-436
; Sequence 436, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
```

CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 436:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-436

Query Match 25.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e-02;
Matches 7; Conservative 0; Mismatches 0; Indels 0;

QY 21 AGTCCAG 27
|||||
Db 1 AGTCCAG 7

RESULT 149
US-08-859-954-437
Sequence 437, Application US/08859954
Patent No. 6083695
GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Homayouni, Ramin
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for
TITLE OF INVENTION: Gene Sequencing and Method Thereof
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 437:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-859-954-437

Query Match 25.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e-02;
Matches 7; Conservative 0; Mismatches 0; Indels 0;

QY 21 AGTCCAG 27
|||||
Db 1 AGTCCAG 7

RESULT 150
US-08-859-954-510/c
Sequence 510, Application US/08859954
Patent No. 6083695
GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Homayouni, Ramin
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Design and Optimized Primer Library for
TITLE OF INVENTION: Gene Sequencing and Method Thereof
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 510:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid

```

; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-859-954-510

Query Match 25.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 AGGGAGT 23
Db 7 AGGGAGT 1

RESULT 151
US-09-878-693-5/c
; Sequence 5, Application US/09878693
; Patent No. 667510
; GENERAL INFORMATION:
; APPLICANT: Windham, Mark T.
; APPLICANT: Trigliano, Robert N.
; APPLICANT: Witte, Willard T.
; TITLE OF INVENTION: Powdery Mildew Resistant Plants
; FILE REFERENCE: UTR-101X
; CURRENT APPLICATION NUMBER: US/09/878,693
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: US 60/210,603
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Random Primer
US-09-878-693-5

Query Match 25.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCTACGT 12
Db 8 CCTACGT 2

RESULT 152
US-08-331-398A-37/c
; Sequence 37, Application US/08331398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
; TITLE OF INVENTION: and Their Uses (as amended)
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,398A
; FILING DATE: 28-OCT-1994
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: 9 base pairs
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-331-398A-37

Query Match 25.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 CAGGGAG 22
Db 9 CAGGGAG 3

RESULT 153
US-08-605-163-11/c
; Sequence 11, Application US/08605163
; Patent No. 5876886
; GENERAL INFORMATION:
; APPLICANT: Meo, Tommaso
; APPLICANT: Tosi, Mario
; APPLICANT: Verpy, Elisabeth
; APPLICANT: Biasotto, Michel
; TITLE OF INVENTION: Method for Detecting Molecules
; TITLE OF INVENTION: Containing Nucleotide Mismatches and the Location of These
; TITLE OF INVENTION: Mismatches, and Application to the Detection of Base
; TITLE OF INVENTION: Substitutions or Deletions in Nucleotide Sequences.
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,163
; FILING DATE: 08-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05986.0005-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs

```

```

; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-859-954-510

Query Match 25.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 AGGGAGT 23
Db 7 AGGGAGT 1

RESULT 151
US-09-878-693-5/c
; Sequence 5, Application US/09878693
; Patent No. 667510
; GENERAL INFORMATION:
; APPLICANT: Windham, Mark T.
; APPLICANT: Trigliano, Robert N.
; APPLICANT: Witte, Willard T.
; TITLE OF INVENTION: Powdery Mildew Resistant Plants
; FILE REFERENCE: UTR-101X
; CURRENT APPLICATION NUMBER: US/09/878,693
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: US 60/210,603
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Random Primer
US-09-878-693-5

Query Match 25.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCTACGT 12
Db 8 CCTACGT 2

RESULT 152
US-08-331-398A-37/c
; Sequence 37, Application US/08331398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
; TITLE OF INVENTION: and Their Uses (as amended)
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,398A
; FILING DATE: 28-OCT-1994
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: 9 base pairs
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-331-398A-37

Query Match 25.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 CAGGGAG 22
Db 9 CAGGGAG 3

RESULT 153
US-08-605-163-11/c
; Sequence 11, Application US/08605163
; Patent No. 5876886
; GENERAL INFORMATION:
; APPLICANT: Meo, Tommaso
; APPLICANT: Tosi, Mario
; APPLICANT: Verpy, Elisabeth
; APPLICANT: Biasotto, Michel
; TITLE OF INVENTION: Method for Detecting Molecules
; TITLE OF INVENTION: Containing Nucleotide Mismatches and the Location of These
; TITLE OF INVENTION: Mismatches, and Application to the Detection of Base
; TITLE OF INVENTION: Substitutions or Deletions in Nucleotide Sequences.
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,163
; FILING DATE: 08-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05986.0005-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs

```

```
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-605-163-11
Query Match      25.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 ACAGGGA 21
Db      8 ACAGGGA 2

RESULT 154
US-08-605-163-12/c
; Sequence 12, Application US/08605163
; Patent No. 5879886
; GENERAL INFORMATION:
; APPLICANT: Meo, Tommaso
; APPLICANT: Tosi, Mario
; APPLICANT: Verpy, Elisabeth
; APPLICANT: Biasotto, Michel
; TITLE OF INVENTION: Method for Detecting Molecules
; TITLE OF INVENTION: Containing Nucleotide Mismatches and the Location of These
; TITLE OF INVENTION: Mismatches, and Application to the Detection of Base
; TITLE OF INVENTION: Substitutions or Deletions in Nucleotide Sequences.
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,163
; FILING DATE: 08-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05986.0005-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-605-163-12

Query Match      25.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 ACAGGGA 21
Db      8 ACAGGGA 2

RESULT 155
US-08-331-397B-37/c
; Sequence 37, Application US/08331397B
; Patent No. 5984726
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
; TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,397B
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,458
; REFERENCE/DOCKET NUMBER: 015280-126120US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-331-397B-37

Query Match      25.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 CAGGGAG 22
Db      9 CAGGGAG 3

RESULT 156
US-08-759-804A-37/c
; Sequence 37, Application US/08759804A
; Patent No. 5990296
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
```



```

; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,804A
; FILING DATE: 03-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,398
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-126140US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-759-804A-37

Query Match 25.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CAGGGAG 22
DB 9 CAGGGAG 3

RESULT 157
US-09-046-858A-3
; Sequence 3, Application US/09046858A
; Patent No. 6048973
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES
; TITLE OF INVENTION: IN ALPHA-AMYLASE GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: PO Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,858A
; FILING DATE: 24-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/042,376

```

```

; FILING DATE: 24-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dehlinger, Peter J.
; REGISTRATION NUMBER: 28,006
; REFERENCE/DOCKET NUMBER: 2000-0456.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0860
; TELEFAX: 650-324-0960
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-046-858A-3

Query Match 25.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTACGTG 13
DB 1 CTACGTG 7

RESULT 158
US-09-227-693-37/C
; Sequence 37, Application US/09227693
; Patent No. 6287562
; GENERAL INFORMATION:
; APPLICANT: PASTAN, Ira
; APPLICANT: BENHAR, Itai
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: JUNG, Sun-Hee
; APPLICANT: LEE, Byungkook
; TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/227,693
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/331,396
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-126-1-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs

```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-227-693-37

Query Match 25.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CAGGGAG 22
| | | | |
DB 9 CAGGGAG 3

RESULT 159

US-09-153-242-33
; Sequence 33, Application US/09153242
; Patent No. 6482592

GENERAL INFORMATION:

; APPLICANT: Lundberg, Joakim
; APPLICANT: Uhlen, Mathias
; TITLE OF INVENTION: MODULAR PROBES II
; FILE REFERENCE: 1181-242
; CURRENT APPLICATION NUMBER: US/09/153,242
; CURRENT FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: PCT/GB97/02629
; FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide H3
US-09-153-242-33

Query Match 25.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGCCCT 8
| | | | |
DB 2 GGGCCCT 8

RESULT 160

US-09-989-789-2121
; Sequence 2121, Application US/09989789
; Patent No. 6588746

GENERAL INFORMATION:

; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2121
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2121

Query Match 25.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CAGGGAG 22
| | | | |
DB 1 CAGGGAG 7

RESULT 161

US-09-989-789-2122
; Sequence 2122, Application US/09989789
; Patent No. 6588746

GENERAL INFORMATION:

; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2122
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2122

Query Match 25.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CAGGGAG 22
| | | | |
DB 1 CAGGGAG 7

RESULT 162

US-09-989-789-2330
; Sequence 2330, Application US/09989789
; Patent No. 6588746

GENERAL INFORMATION:

; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2330
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2330

Query Match 25.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGAGTCC 25
| | | | |
DB 3 GGAGTCC 9

RESULT 163

US-09-989-789-2331
; Sequence 2331, Application US/09989789
; Patent No. 6588746

GENERAL INFORMATION:

```
/ APPLICANT: LIU, Qiang
/ TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
/ FILE REFERENCE: 8325-0011.20 / S11-US2
/ CURRENT APPLICATION NUMBER: US/09/989,789
/ CURRENT FILING DATE: 2002-03-25
/ NUMBER OF SEQ ID NOS: 4085
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 2331
/ LENGTH: 9
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: example target
/ OTHER INFORMATION: DNA
US-09-989-789-2331

Query Match      25.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGAGTCC 25
Db 3 GGAGTCC 9

RESULT 164
US-09-989-789-2347
/ Sequence 2347, Application US/09989789
/ Patent No. 6588746
/ GENERAL INFORMATION:
/ APPLICANT: LIU, Qiang
/ TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
/ FILE REFERENCE: 8325-0011.20 / S11-US2
/ CURRENT APPLICATION NUMBER: US/09/989,789
/ CURRENT FILING DATE: 2002-03-25
/ NUMBER OF SEQ ID NOS: 4085
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 2347
/ LENGTH: 9
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: example target
/ OTHER INFORMATION: DNA
US-09-989-789-2347

Query Match      25.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGAGTCC 25
Db 3 GGAGTCC 9

RESULT 165
US-09-989-789-2348
/ Sequence 2348, Application US/09989789
/ Patent No. 6588746
/ GENERAL INFORMATION:
/ APPLICANT: LIU, Qiang
/ TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
/ FILE REFERENCE: 8325-0011.20 / S11-US2
/ CURRENT APPLICATION NUMBER: US/09/989,789
/ CURRENT FILING DATE: 2002-03-25
/ NUMBER OF SEQ ID NOS: 4085
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 2348
/ LENGTH: 9
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: example target
/ OTHER INFORMATION: DNA
US-09-989-789-2348

Query Match      25.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGAGTCC 25
Db 3 GGAGTCC 9

RESULT 166
US-09-450-515-3
/ Sequence 3, Application US/09450515
/ Patent No. 6680425
/ GENERAL INFORMATION:
/ APPLICANT: Rodriguez, Raymond L.
/ TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES
/ IN ALPHA-AMYLASE GENES
/ NUMBER OF SEQUENCES: 21
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Dehlinger & Associates
/ STREET: PO Box 60850
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94306
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: PastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/450,515
/ FILING DATE: 29-No. 6680425-1999
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/046,858
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Dehlinger, Peter J.
/ REGISTRATION NUMBER: 28,006
/ REFERENCE/DOCKET NUMBER: 2000-0456.30
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-324-0880
/ TELEFAX: 650-324-0960
/ TELEX: <Unknown>
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-450-515-3

Query Match      25.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTACGTG 13
Db 1 CTACGTG 7

RESULT 167
US-09-263-790-19/c
/ Sequence 19, Application US/09263790
/ Patent No. PPI2997
```

```
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: example target
/ OTHER INFORMATION: DNA
US-09-989-789-2348

Query Match      25.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGAGTCC 25
Db 3 GGAGTCC 9

RESULT 166
US-09-450-515-3
/ Sequence 3, Application US/09450515
/ Patent No. 6680425
/ GENERAL INFORMATION:
/ APPLICANT: Rodriguez, Raymond L.
/ TITLE OF INVENTION: SUGAR-REGULATORY SEQUENCES
/ IN ALPHA-AMYLASE GENES
/ NUMBER OF SEQUENCES: 21
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Dehlinger & Associates
/ STREET: PO Box 60850
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94306
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: PastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/450,515
/ FILING DATE: 29-No. 6680425-1999
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/046,858
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Dehlinger, Peter J.
/ REGISTRATION NUMBER: 28,006
/ REFERENCE/DOCKET NUMBER: 2000-0456.30
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-324-0880
/ TELEFAX: 650-324-0960
/ TELEX: <Unknown>
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-450-515-3

Query Match      25.0%; Score 7; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTACGTG 13
Db 1 CTACGTG 7

RESULT 167
US-09-263-790-19/c
/ Sequence 19, Application US/09263790
/ Patent No. PPI2997
```

```

; GENERAL INFORMATION:
; APPLICANT: Nirmal Kumar PATRA et al.
; TITLE OF INVENTION: JAL PALLAVI, WATER LOGGING TOLERANT CYMBOPOGON WINTERIANUS
; FILE REFERENCE: 2761-0120P
; CURRENT APPLICATION NUMBER: US/09/263,790
; CURRENT FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: MAP 19 Primer - Primer used in RAPD analysis comparing Jal Pallav
; OTHER INFORMATION: with Jorlab-2, Marjusha, Mandakini, Bio-13, and Ceylon.
US-09-263-790-19

Query Match      25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 GGAGTCC 25
Db 7 GGAGTCC 1

RESULT 168
US-09-538-341-12/c
; Sequence 12, Application US/09538341
; Patent No. PP13110
; GENERAL INFORMATION:
; APPLICANT: Kumar, Sushil
; APPLICANT: Bahl, Janak Raj
; APPLICANT: Bansal, Ravi Prakash
; APPLICANT: Niwas, Shri
; APPLICANT: Naqvi, Arif Ali
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Shasany, Ajit Kumar
; APPLICANT: Darokar, Mahendra Pandurang
; APPLICANT: Singh, Vikram
; APPLICANT: Sinha, Shweta
; TITLE OF INVENTION: Lippia alba plant named 'Bhurakshak'
; FILE REFERENCE: U-012701-4
; CURRENT APPLICATION NUMBER: US/09/538,341
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 12
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for generating random amplified polymorphic DNA profile of
; OTHER INFORMATION: plant
US-09-538-341-12

Query Match      25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 GGAGTCC 25
Db 7 GGAGTCC 1

RESULT 169
US-09-785-716A-18/c
; Sequence 18, Application US/09785716A
; Patent No. PP14090
; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; APPLICANT: Dwivedi, Samresh
; APPLICANT: Singh, Maneesha
; APPLICANT: Singh, Ajay Pratap
; APPLICANT: Singh, Vandana
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Naqvi, Ali Arif
; APPLICANT: Kuman, Sushil
; TITLE OF INVENTION: New Peppermint Plant Named 'PRANJAL'
; FILE REFERENCE: 41799/VGG/K375
; CURRENT APPLICATION NUMBER: US/09/785,716A
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for RAPD profile
US-09-785-716A-18

Query Match      25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 GGAGTCC 25
Db 7 GGAGTCC 1

RESULT 170
US-09-799-880-19/c
; Sequence 19, Application US/09799880
; Patent No. PP14400
; GENERAL INFORMATION:
; APPLICANT: Gupta, Ritika
; APPLICANT: Sastri, Kakaraparthi
; APPLICANT: Banerjee, Suchitra
; APPLICANT: Mallavarapu, Gopal
; APPLICANT: Ramesh, Srinivas
; APPLICANT: Shasany, Ajit
; APPLICANT: Darokar, Mahendra
; APPLICANT: Khanuja, Suman
; TITLE OF INVENTION: A NOVEL ROSE SCENTED GERANIUM PELARGONIUM GRAVEOLENS PLANT 'SAF'
; FILE REFERENCE: 2734-102
; CURRENT APPLICATION NUMBER: US/09/799,880
; CURRENT FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-799-880-19

Query Match      25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 GGAGTCC 25
Db 7 GGAGTCC 1

RESULT 171
US-08-590-571-19/c
; Sequence 19, Application US/08590571
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Nallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; City: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/590,571
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: Yale
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-590-571-19
;
; Query Match 25.0%; Score 7; DB 1; Length 10;
; Best Local Similarity 100.0%; Pred. No. 85;
; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 18 GGGAGTC 24
Db 9 GGGAGTC 3
;
; RESULT 172
; US-08-590-571-31/c
; Sequence 31, Application US/08590571
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Nallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; City: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/590,571
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: Yale
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:

```

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; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-590-571-31
;
; Query Match 25.0%; Score 7; DB 1; Length 10;
; Best Local Similarity 100.0%; Pred. No. 85;
; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 18 GGGAGTC 24
Db 9 GGGAGTC 3
;
; RESULT 173
; US-08-388-353-659/c
; Sequence 659, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; City: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 659:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-659
;
; Query Match 25.0%; Score 7; DB 1; Length 10;
; Best Local Similarity 100.0%; Pred. No. 85;
; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 13 GTACAGG 19
Db 8 GTACAGG 2
;
; RESULT 174
; US-08-388-353-660/c
; Sequence 660, Application US/08388353

```

```

; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 660:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs.
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-660

Query Match 25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GTACAGG 19
Db 7 GTACAGG 1

RESULT 175
US-08-468-856B-14
; Sequence 14, Application US/08468856B
; Patent No. 6013772
; GENERAL INFORMATION:
; APPLICANT: Barnett, Thomas; Elting, James; Kamarch, Michael;
; APPLICANT: Kretschmer, Axel
; TITLE OF INVENTION: CDNAS CODING FOR MEMBERS OF THE
; TITLE OF INVENTION: CARCINOEMBRYONIC ANTIGEN FAMILY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spring Horn Kramer & Woods
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 Mb storage
; COMPUTER: APPLE MACINTOSH 6500
; OPERATING SYSTEM: SYSTEM 7.5
; SOFTWARE: WordPerfect 3.5

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,856B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/027,974
; FILING DATE: 08-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/760,031
; FILING DATE: 13-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/274,107
; FILING DATE: 21-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/207,678
; FILING DATE: 16-JUN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/060,031
; FILING DATE: 19-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/016,683
; FILING DATE: 19-FEB-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/896,361
; FILING DATE: 13-AUG-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: MDI 242.10-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-468-856B-14

Query Match 25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGCCCT 8
Db 1 GGGCCCT 7

RESULT 176
US-08-488-551B-659/c
; Sequence 659, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B

```

;/ FILING DATE: 07-JUN-1995
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: PM3864 (AU)
;/ FILING DATE: 14-FEB-1994
;/ APPLICATION NUMBER: PM4002 (AU)
;/ FILING DATE: 21-FEB-1994
;/ APPLICATION NUMBER: PM0284 (AU)
;/ FILING DATE: 23-DEC-1994
;/ APPLICATION NUMBER: US 08/388,353
;/ FILING DATE: 14-FEB-1995
;/ APPLICATION NUMBER: PM3021/95
;/ FILING DATE: 17-MAY-1995
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: FRANK S. DIGIGLIO
;/ REFERENCE/DOCKET NUMBER: 9606Z
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (516) 742-4343
;/ TELEFAX: (516) 742-4366
;/ INFORMATION FOR SEQ ID NO: 659:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 10 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: DNA
;/ US-08-488-551B-659

Query Match 25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GTACAGG 19
Db 8 GTACAGG 2

RESULT 177
US-08-488-551B-660/C
; Sequence 660, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:

;/ NAME: FRANK S. DIGIGLIO
;/ REFERENCE/DOCKET NUMBER: 9606Z
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (516) 742-4343
;/ TELEFAX: (516) 742-4366
;/ INFORMATION FOR SEQ ID NO: 660:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 10 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: DNA
;/ US-08-488-551B-660

Query Match 25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GTACAGG 19
Db 7 GTACAGG 1

RESULT 178
US-08-468-859A-14
; Sequence 14, Application US/08468859A
; Patent No. 602358
; GENERAL INFORMATION:
; APPLICANT: Barnett, Thomas; Elting, James; Kamarck, Michael;
; APPLICANT: Kretschmer, Axel
; TITLE OF INVENTION: CDNAS CODING FOR MEMBERS OF THE
; TITLE OF INVENTION: CARCINOEMBRYONIC ANTIGEN FAMILY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sprung Horn Kramer & Woods
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 Mb storage
; COMPUTER: APPLE MACINTOSH 6500
; OPERATING SYSTEM: SYSTEM 7.5
; SOFTWARE: WordPerfect 3.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,859A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/027,974
; FILING DATE: 08-MAR-1993
; APPLICATION NUMBER: US 07/760,031
; FILING DATE: 13-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/274,107
; FILING DATE: 21-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/207,678
; FILING DATE: 16-JUN-1988
; APPLICATION NUMBER: US 07/060,031
; FILING DATE: 19-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/016,683
; FILING DATE: 19-FEB-1987
; APPLICATION NUMBER: US 06/896,361
; FILING DATE: 13-AUG-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141

; REFERENCE/DOCKET NUMBER: MDI 242.9-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-468-859A-14

Query Match 25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGCCCT 8
DB 1 GGGCCCT 7

RESULT 179
US-08-906-691-10/c
; Sequence 10, Application US/08906691
; Patent No. 6066452
; GENERAL INFORMATION:
; APPLICANT: Weisman, Sherman M.
; APPLICANT: Nallur, Girish N.
; APPLICANT: Kulkarni, Prakash
; TITLE OF INVENTION: MULTIPLEX SELECTION TECHNIQUE FOR
; IDENTIFYING PROTEIN-BINDING SITES FOR DNA-BINDING PROTEINS
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 981094
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,691
; FILING DATE: 31-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6066452tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 390036.403C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-906-691-10

Query Match 25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGGAGTC 24
DB 9 GGGAGTC 3

RESULT 180
US-08-522-384-27/c
; Sequence 27, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; CHARACTERIZING NUCLEOTIDE SEQUENCES
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-27

Query Match 25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GTCCAGG 28
DB 7 GTCCAGG 1

RESULT 181
US-09-154-750A-49
; Sequence 49, Application US/09154750A
; Patent No. 6432640
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; CURRENT FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/059,153
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079817
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-154-750A-49

Query Match 25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 AGGAGT 23
DB 2 AGGAGT 8

RESULT 182
US-09-313-221A-136/c
; Sequence 136, Application US/09313221A
; Patent No. 6468743
; GENERAL INFORMATION:
; APPLICANT: Thomas L. Romick (Inventor)
; APPLICANT: Mark S. Fraser (Inventor)
; TITLE OF INVENTION: PCR TECHNIQUES FOR DETECTING MICROBIAL
; AND VIRAL CONTAMINANTS IN FOODSTUFFS


```
; SEQ ID NO 9
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-538-456-9

Query Match      25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGAGTCC 25
    |||||
Db 7 GGAGTCC 1

RESULT 187
US-09-769-482-43
; Sequence 43, Application US/09769482
; Patent No. 6566130
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
; FILE REFERENCE: 04995.0057-00000
; CURRENT APPLICATION NUMBER: US/09769,482
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-769-482-43

Query Match      25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CAGGAG 22
    |||||
Db 3 CAGGAG 9

RESULT 188
US-09-989-789-1285
; Sequence 1285, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1285
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1314

Query Match      25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGCCCT 8
    |||||
Db 2 GGGCCCT 8

RESULT 189
US-09-989-789-1307
; Sequence 1307, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1307
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1307

Query Match      25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGCCCT 8
    |||||
Db 2 GGGCCCT 8

RESULT 190
US-09-989-789-1314
; Sequence 1314, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1314
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1314

Query Match      25.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGCCCT 8
    |||||
Db 2 GGGCCCT 8
```

```
RESULT 191
US-09-263-790-19
; Sequence 19, Application US/09263790
; Patent No. PPI2997
; GENERAL INFORMATION:
; APPLICANT: Nital Kumar PATRA et al.
; TITLE OF INVENTION: JAL PALLAVI, WATER LOGGING TOLERANT CYMBOPOGON WINTERIANUS
; FILE REFERENCE: 2761-0120P
; CURRENT APPLICATION NUMBER: US/09/263,790
; CURRENT FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 19
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: with Joriab-2, Manjusha, Mandakini, Bio-13, and Ceylon.
US-09-263-790-19

Query Match      24.3%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

QY 19 GGAGTCCAGG 28
DB 1 GGACTCCAGC 10

RESULT 192
US-09-538-341-12
; Sequence 12, Application US/09538341
; Patent No. PPI3110
; GENERAL INFORMATION:
; APPLICANT: Kumar, Sushil
; APPLICANT: Bahl, Janak Faj
; APPLICANT: Bansal, Ravi Prakash
; APPLICANT: Niwas, Shri
; APPLICANT: Naqvi, Arif Ali
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Shasany, Ajit Kumar
; APPLICANT: Darokar, Mahendra Pandurang
; APPLICANT: Singh, Vikram
; APPLICANT: Sinha, Shweta
; TITLE OF INVENTION: Lippia alba plant named 'Bhurakshak'
; FILE REFERENCE: U-012701-4
; CURRENT APPLICATION NUMBER: US/09/538,341
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 12
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for generating random amplified polymorphic DNA profile of
US-09-538-341-12

Query Match      24.3%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

QY 19 GGAGTCCAGG 28
DB 1 GGACTCCAGC 10

RESULT 193
US-09-785-716A-18
; Sequence 18, Application US/09785716A
```

```
; Patent No. PPI4090
; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; APPLICANT: Dwivedi, Samresh
; APPLICANT: Singh, Maneesha
; APPLICANT: Singh, Ajay Pratap
; APPLICANT: Singh, Vandana
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Naqvi, Ali Arif
; APPLICANT: Kuman, Sushil
; TITLE OF INVENTION: New Peppermint Plant Named 'PRANJAL'
; FILE REFERENCE: 41799/VGG/K375
; CURRENT APPLICATION NUMBER: US/09/785,716A
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 18
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for RAPD profile
US-09-785-716A-18

Query Match      24.3%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 19 GGAGTCCAGG 28
DB 1 GGACTCCAGC 10

RESULT 194
US-09-799-980-19
; Sequence 19, Application US/09799880
; Patent No. PPI4400
; GENERAL INFORMATION:
; APPLICANT: Kumar, Sushil
; APPLICANT: Gupta, Ritika
; APPLICANT: Sastri, Kakaraparthi
; APPLICANT: Banerjee, Suchitra
; APPLICANT: Mallavarapu, Gopal
; APPLICANT: Ramesh, Srinivas
; APPLICANT: Shasany, Ajit
; APPLICANT: Darokar, Mahendra
; APPLICANT: Khanuja, Suman
; TITLE OF INVENTION: A NOVEL ROSE SCENTED GERANIUM PELARGONIUM GRAVEOLENS PLANT 'SAF'
; FILE REFERENCE: 2734-102
; CURRENT APPLICATION NUMBER: US/09/799,880
; CURRENT FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 19
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-799-980-19

Query Match      24.3%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 19 GGAGTCCAGG 28
DB 1 GGACTCCAGC 10

RESULT 195
US-08-388-353-660
; Sequence 660, Application US/08388353
```

```
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Leamont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 660:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-660

Query Match 24.3%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CGGTGACAGG 19
Db 1 CCTGTACTGG 10

RESULT 196
US-08-488-551B-660
; Sequence 660, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

Query Match 24.3%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CGGTGACAGG 19
Db 1 CCTGTACTGG 10

RESULT 197
US-09-537-186-13
; Sequence 13, Application US/09537186
; Patent No. 6534696
; GENERAL INFORMATION:
; APPLICANT: COUNCIL OF SCIENTIFIC AND INDUSTRIAL RESEARCH
; TITLE OF INVENTION: A disease resistant high yielding variety Papaver somniferum cal
; FILE OF INVENTION: Rakshit
; FILE REFERENCE: Q58615
; CURRENT APPLICATION NUMBER: US/09/537,186
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: : Primer for generating ran
; OTHER INFORMATION: m amplified polymorphic DNA profile of claimed plant
; US-09-537-186-13

Query Match 24.3%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 19 GGAGTCCAGG 28
Db 1 GGAGTCCAGG 10

RESULT 198
US-09-538-456-9
; Sequence 9, Application US/09538456
; Patent No. 6558940
```

```

; GENERAL INFORMATION:
; APPLICANT: Alam, Mansoor
; APPLICANT: Sattar, Abdul
; APPLICANT: Kumar, Sushil
; APPLICANT: Samad, Abdul
; APPLICANT: Dhawan, Om Prakash
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Shasany, Ajit Kumar
; APPLICANT: Singh, Seena
; APPLICANT: Kumar, Poovappallivadakethil Viswanathan Nair Ajay
; APPLICANT: Khalique, Abdul
; APPLICANT: Zaim, Mohammad
; APPLICANT: Shahabuddin, Saba
; APPLICANT: Trivedi, Mala
; TITLE OF INVENTION: A novel Streptomyces strain with potential anti-microbial
; TITLE OF INVENTION: activity against phytopathogenic fungi
; FILE REFERENCE: 148920.00003
; CURRENT APPLICATION NUMBER: US/09/538,456
; CURRENT FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Microsoft Word-97
; SEQ ID NO 9
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: primer
; US-09-538-456-9

Query Match      24.3%; Score 6.8; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 19 GGAGTCCAGG 28
Db 1 GGACTCCAGG 10

; GENERAL INFORMATION:
; APPLICANT: Koinick, Mark H. Alexander
; APPLICANT: Cannon-Albright, Lisa A.
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,177
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03537
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994

```

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-474-177-23

Query Match      23.6%; Score 6.6; DB 1; Length 16;
Best Local Similarity 69.2%; Pred. No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CTAGGTGTACAGG 19
Db 13 CTTCTGTGACAG 1

; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1E1-Beta GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,033
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086

```

```

RESULT 199
US-08-474-177-23/c
; Sequence 23, Application US/08474177
; Patent No. 5624819
; GENERAL INFORMATION:
; APPLICANT: Koinick, Mark H. Alexander
; APPLICANT: Cannon-Albright, Lisa A.
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,177
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03537
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994

```

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RESULT 200
US-08-487-033-23/c
; Sequence 23, Application US/08487033
; Patent No. 5739027
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1E1-Beta GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,033
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086

```

;/ FILING DATE: 18-MAR-1994
;/ PRIOR APPLICATION NUMBER: US 08/227,369
;/ FILING DATE: 14-APR-1994
;/ PRIOR APPLICATION DATA:
;/ FILING DATE: 18-MAR-1994
;/ PRIOR APPLICATION NUMBER: US 08/214,582
;/ FILING DATE: 18-MAR-1994
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Ihnen, Jeffrey L.
;/ REGISTRATION NUMBER: 28,957
;/ REFERENCE/DOCKET NUMBER: 24884-109348-C
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 202-962-4810
;/ TELEFAX: 202-962-8300
;/ INFORMATION FOR SEQ ID NO: 23:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 16 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: DNA (genomic)
;/ HYPOTHETICAL: NO
;/ ANTI-SENSE: YES
;/ ORIGINAL SOURCE:
;/ ORGANISM: Homo sapiens
;/ US-08-487-033-23
;
Query Match 23.6%; Score 6.6; DB 1; Length 16;
Best Local Similarity 69.2%; Pred. No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 7 CTACGTGTACAGG 19
Db 13 CTTCCTGGACACG 1

RESULT 201
US-08-480-810-23/c
; Sequence 23, Application US/08480810
; Patent No. 5801236
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US/08/480,810
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:

;/ APPLICATION NUMBER: US 08/227,369
;/ FILING DATE: 14-APR-1994
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/214,582
;/ FILING DATE: 18-MAR-1994
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Ihnen, Jeffrey L.
;/ REGISTRATION NUMBER: 28,957
;/ REFERENCE/DOCKET NUMBER: 24884-109348
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 202-962-4810
;/ TELEFAX: 202-962-8300
;/ INFORMATION FOR SEQ ID NO: 23:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 16 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: DNA (genomic)
;/ HYPOTHETICAL: NO
;/ ANTI-SENSE: YES
;/ ORIGINAL SOURCE:
;/ ORGANISM: Homo sapiens
;/ US-08-480-810-23
;
Query Match 23.6%; Score 6.6; DB 1; Length 16;
Best Local Similarity 69.2%; Pred. No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 7 CTACGTGTACAGG 19
Db 13 CTTCCTGGACACG 1

RESULT 202
US-08-508-735-23/c
; Sequence 23, Application US/08508735
; Patent No. 5843756
; GENERAL INFORMATION:
; APPLICANT: Stone, Steven
; APPLICANT: Jiang, Ping
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/508,735
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US to be assigned
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
;/ REGISTRATION NUMBER: 28,957
;/ REFERENCE/DOCKET NUMBER: 24884-109348
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 202-962-4848
;/ TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-508-735-23

Query Match 23.6%; Score 6.6; DB 1; Length 16;
Best Local Similarity 69.2%; Pred. No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGG 19
Db 13 CTTCTGGACACG 1

RESULT 203

US-08-848-251-23/c
Sequence 23, Application US/08848251
Patent No. 5989815

GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND
TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS
TITLE OF INVENTION: GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,251
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/474,083
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24884-109348-G
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-848-251-23

Query Match 23.6%; Score 6.6; DB 1; Length 16;
Best Local Similarity 69.2%; Pred. No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGG 19
Db 13 CTTCTGGACACG 1

RESULT 204

US-08-486-047-23/c
Sequence 23, Application US/08486047
Patent No. 5994095

GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS2 GENE
TITLE OF INVENTION: GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,047
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-B
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-486-047-23

Query Match 23.6%; Score 6.6; DB 1; Length 16;
Best Local Similarity 69.2%; Pred.No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGG 19
DB 13 CTTCTGGACAG 1

RESULT 205

US-09-120-130-23/c
Sequence 23, Application US/09120130

Patent No. 6037462

GENERAL INFORMATION:

APPLICANT: Kamb, Alexander

TITLE OF INVENTION: MTS1 GENE

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/120,130

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/480,810

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/251,938

FILING DATE: 01-JUN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/215,087

FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/215,086

FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/227,369

FILING DATE: 14-APR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/214,582

FILING DATE: 18-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24884-109348

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-962-4810

TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-120-130-23

Query Match 23.6%; Score 6.6; DB 1; Length 16;
Best Local Similarity 69.2%; Pred.No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGG 19
DB 13 CTTCTGGACAG 1

RESULT 206

US-09-115-252-23/c

Sequence 23, Application US/09115252

Patent No. 6080301

GENERAL INFORMATION:

APPLICANT: Kamb, Alexander

TITLE OF INVENTION: MTS1 GENE

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP

STREET: 1201 New York Avenue, Suite 1000

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/115,252

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/480,810

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: PCI/US95/03316

FILING DATE: 17-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/251,938

FILING DATE: 01-JUN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/215,087

FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/215,086

FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/227,369

FILING DATE: 14-APR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/214,582

FILING DATE: 18-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24884-109348

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-962-4810

TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-115-252-23

Query Match 23.6%; Score 6.6; DB 1; Length 16;
Best Local Similarity 69.2%; Pred. No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGG 19
DB 13 CTTCTGGACAG 1

RESULT 207

US-08-986-515-23/c
Sequence 23, Application US/08986515
Patent No. 6090578

GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS1 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986.515
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,810
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:

LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-986-515-23

Query Match 23.8%; Score 6.6; DB 1; Length 16;
Best Local Similarity 69.2%; Pred. No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGG 19
DB 13 CTTCTGGACAG 1

RESULT 208

US-09-120-128-23/c
Sequence 23, Application US/09120128
Patent No. 6140473

GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS2 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/120,128
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/486,047
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:

LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-120-128-23

Query Match 23.6%; Score 6.6; DB 1; Length 16;
Best Local Similarity 69.2%; Pred No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy 7 CTACGTGTACAGG 19
Db 13 CTTCTGGACAGC 1

RESULT 209

US-09-120-129-23/c
Sequence 23, Application US/09120129
Patent No. 6180776
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS2 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/120,129
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,047
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:

LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-120-129-23

Query Match 23.6%; Score 6.6; DB 1; Length 16;
Best Local Similarity 69.2%; Pred No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy 7 CTACGTGTACAGG 19
Db 13 CTTCTGGACAGC 1

RESULT 210

US-09-201-139-23/c
Sequence 23, Application US/09201139
Patent No. 6210949
GENERAL INFORMATION:
APPLICANT: Stone, Steven
TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,139
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/508,735
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4848
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-201-139-23

Query Match

23.6%; Score 6.6; DB 1; Length 16;

Best Local Similarity 69.2%; Pred. No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CTAGGTGTACAGG 19
||| ||| ||| ||| |||
Db 13 CTTCTGGACAG 1

RESULT 211
US-09-120-131-23/c
; Sequence 23, Application US/09120131
; Patent No. 6218146
; GENERAL INFORMATION:
; APPLICANT: Ramb, Alexander
; TITLE OF INVENTION: MTS2 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/120,131
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/486,047
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-120-131-23

Query Match 23.6%; Score 6.6; DB 1; Length 16;

Best Local Similarity 69.2%; Pred. No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CTAGGTGTACAGG 19
||| ||| ||| ||| |||
Db 13 CTTCTGGACAG 1

RESULT 212
US-08-522-384-34
; Sequence 34, Application US/08522384
; Patent No. 6118667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-34

Query Match 22.9%; Score 6.4; DB 1; Length 10;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CGTGCTACA 17
||| ||| ||| ||| |||
Db 3 CATGTACA 10

RESULT 213
US-09-425-798-12
; Sequence 12, Application US/09425798A
; Patent No. 6423493
; GENERAL INFORMATION:
; APPLICANT: Gorenstein Dr., David G.
; APPLICANT: King Dr., David J.
; APPLICANT: Ventura, Daniel A.
; APPLICANT: Brasier Dr., Allan R.
; TITLE OF INVENTION: Combinatorial Selection of Phosphothionate
; Oligonucleotide Aptamers
; FILE REFERENCE: 122144-1005
; CURRENT APPLICATION NUMBER: US/09/425,798A
; CURRENT FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 60/105,600
; PRIOR FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: aptamer
US-09-425-798-12

Query Match 22.9%; Score 6.4; DB 1; Length 10;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 TGTACAGG 19
||| ||| ||| ||| |||
Db 3 TGTACATG 10

RESULT 214
US-08-319-492B-24/C
; Sequence 24, Application US/09319492B
; Patent No. 5616488
; GENERAL INFORMATION:
; APPLICANT: Sullivan, Sean M.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: RBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF IL-5
; NUMBER OF SEQUENCES: 751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,492B
; FILING DATE: October 7, 1994
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/276
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-319-492B-24

Query Match 22.1%; Score 6.2; DB 1; Length 15;
Best Local Similarity 72.7%; Pred. No. 2e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 TACAGGAGTC 24
|||
Db 14 TACAGTAGGC 4

RESULT 215
US-09-989-789-2453
; Sequence 2453, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789

; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2453
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2453

Query Match 21.4%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e-02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGCCC 7
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Db 3 GGGCCC 8

RESULT 216
US-09-989-789-2454
; Sequence 2454, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2454
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2454

Query Match 21.4%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e-02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGCCC 7
|||
Db 3 GGGCCC 8

RESULT 217
US-09-153-242-30/C
; Sequence 30, Application US/09153242
; Patent No. 6482592
; GENERAL INFORMATION:
; APPLICANT: Lundberg, Joakim
; APPLICANT: Uhlen, Mathias
; TITLE OF INVENTION: MODULAR PROBES II
; FILE REFERENCE: 1181-242
; CURRENT APPLICATION NUMBER: US/09/153,242
; CURRENT FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: PCT/GB97/02629
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: oligonucleotide H1-9
US-09-153-242-30

Query Match 21.4%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e-02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGCCC 7
| | | | |
Db 6 GGGCCC 1

RESULT 218

US-09-153-242-33/c
; Sequence 33, Application US/09153242
; Patent No. 6482592
; GENERAL INFORMATION:
; APPLICANT: Lundberg, Joakim
; TITLE OF INVENTION: MODULAR PROBES II
; FILE REFERENCE: 1181-242
; CURRENT APPLICATION NUMBER: US/09/153,242
; CURRENT FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: PCT/GB97/02629
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide H3
US-09-153-242-33

Query Match 21.4%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e-02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGCCC 7
| | | | |
Db 7 GGGCCC 2

Search completed: April 19, 2004, 15:06:49
Job time : 1 secs

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2004, 15:10:53 ; Search time 0.001 Seconds

(without alignments)
68.488 Million cell updates/sec

Title: US-10-024-396-3-COPY

Perfect score: 28

Sequence: 1 cgggcctacgtgtacaggagtcagg 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 95 seqs, 1223 residues

Total number of hits satisfying chosen parameters: 190

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 132 summaries

Database : pbdb:*

Published - Applications - NA

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	71.4	20	1	US-10-024-396-19
C 2	20	71.4	20	1	US-10-024-396-20
C 3	14.2	50.7	19	1	US-08-983-605-203
C 4	14.2	50.7	21	1	US-09-853-105-19
C 5	13.4	47.9	20	1	US-09-918-779-35
C 6	13.2	47.1	20	1	US-10-159-856-39
C 7	13.2	47.1	20	1	US-10-159-856-105
C 8	12.4	44.3	19	1	US-10-184-372-23
C 9	12.2	43.6	17	1	US-09-882-945A-275
C 10	11.4	40.7	17	1	US-09-930-423-643
C 11	11.4	40.7	17	1	US-09-930-423-1045
C 12	11.4	40.7	17	1	US-09-930-423-1120
C 13	11.4	40.7	17	1	US-09-745-237A-643
C 14	11.4	40.7	17	1	US-09-745-237A-1045
C 15	11.4	40.7	17	1	US-09-745-237A-1120
C 16	11.2	40.0	17	1	US-09-818-875-2950
C 17	11.2	40.0	17	1	US-09-818-875-2951
C 18	11.2	40.0	17	1	US-10-156-306-7026
C 19	11.2	40.0	17	1	US-10-156-306-7027
C 20	11.2	40.0	17	1	US-10-238-700-3087
C 21	11.2	40.0	17	1	US-10-209-787-2950
C 22	11.2	40.0	17	1	US-10-209-787-2951
C 23	11.2	40.0	17	1	US-10-261-185-2950
C 24	11.2	40.0	17	1	US-10-261-185-2951
C 25	10.8	38.6	15	1	US-09-504-231A-143
C 26	10.8	38.6	15	1	US-09-504-231A-143
C 27	10.4	37.1	12	1	US-10-407-637-20
C 28	10.2	36.4	15	1	US-09-879-813-73
C 29	10.2	36.4	15	1	US-09-912-673A-55
C 30	10.2	36.4	15	1	US-10-146-505-73
C 31	10.2	36.4	15	1	US-10-193-507-83
C 32	10	35.7	10	1	US-09-504-231A-319
C 33	10	35.7	15	1	US-09-274-553D-319

34	10	35.7	15	1	US-10-193-507-51	Sequence 51, Appl
35	9.8	35.0	14	1	US-08-591-486B-61	Sequence 61, Appl
36	9.8	35.0	15	1	US-05-504-231A-137	Sequence 137, Appl
37	9.8	35.0	15	1	US-09-274-553D-137	Sequence 137, Appl
38	9.8	35.0	15	1	US-10-113-877-35	Sequence 35, Appl
39	9.4	33.6	12	1	US-09-989-364-67	Sequence 67, Appl
C 40	9.2	32.9	14	1	US-08-591-486B-164	Sequence 164, Appl
C 41	9	32.1	10	1	US-10-330-627-29	Sequence 29, Appl
C 42	8.8	31.4	12	1	US-09-989-364-67	Sequence 67, Appl
C 43	8.8	31.4	13	1	US-10-104-307-26	Sequence 26, Appl
C 44	8.4	30.0	10	1	US-09-851-871-85	Sequence 85, Appl
C 45	8.4	30.0	10	1	US-10-329-465-242	Sequence 242, Appl
C 46	8.4	30.0	10	1	US-10-330-045-14	Sequence 14, Appl
C 47	8.4	30.0	10	1	US-10-330-627-1257	Sequence 1257, Appl
C 48	8.4	30.0	10	1	US-10-438-583-7	Sequence 7, Appl
C 49	8.4	30.0	10	1	US-10-444-206-85	Sequence 85, Appl
C 50	8.4	30.0	11	1	US-09-249-155-45	Sequence 45, Appl
C 51	8.4	30.0	11	1	US-09-851-871-86	Sequence 86, Appl
C 52	8.4	30.0	11	1	US-10-314-322-45	Sequence 45, Appl
C 53	8.4	30.0	11	1	US-10-444-206-86	Sequence 86, Appl
C 54	8.4	30.0	12	1	US-09-851-871-87	Sequence 87, Appl
C 55	8.4	30.0	12	1	US-10-444-206-87	Sequence 87, Appl
C 56	8.2	29.3	17	1	US-10-238-700-3087	Sequence 3087, Appl
C 57	8.2	29.3	20	1	US-10-024-396-19	Sequence 19, Appl
C 58	8.2	29.3	20	1	US-09-853-105-19	Sequence 19, Appl
C 59	8.2	29.3	21	1	US-09-989-789-2098	Sequence 2098, Appl
C 60	8	28.6	9	1	US-09-989-789-2100	Sequence 2100, Appl
C 61	8	28.6	9	1	US-09-989-789-2195	Sequence 2195, Appl
C 62	8	28.6	9	1	US-09-989-789-2453	Sequence 2453, Appl
C 63	8	28.6	9	1	US-09-989-789-2454	Sequence 2454, Appl
C 64	8	28.6	9	1	US-09-989-789-2454	Sequence 2454, Appl
C 65	8	28.6	9	1	US-09-989-789-2454	Sequence 2454, Appl
C 66	8	28.6	9	1	US-09-989-789-2454	Sequence 2454, Appl
C 67	8	28.6	9	1	US-09-989-789-2454	Sequence 2454, Appl
C 68	8	28.6	9	1	US-09-989-789-2454	Sequence 2454, Appl
C 69	8	28.6	9	1	US-09-989-789-2454	Sequence 2454, Appl
C 70	8	28.6	9	1	US-09-989-789-2454	Sequence 2454, Appl
C 71	8	28.6	9	1	US-09-989-789-2454	Sequence 2454, Appl
C 72	8	28.6	9	1	US-09-989-789-2454	Sequence 2454, Appl
C 73	8	28.6	9	1	US-09-989-789-2454	Sequence 2454, Appl
C 74	8	28.6	9	1	US-09-989-789-2454	Sequence 2454, Appl
C 75	8	28.6	9	1	US-09-989-789-2454	Sequence 2454, Appl
C 76	8	28.6	9	1	US-09-989-789-2454	Sequence 2454, Appl
C 77	8	28.6	9	1	US-09-989-789-2454	Sequence 2454, Appl
C 78	8	28.6	9	1	US-09-989-789-2454	Sequence 2454, Appl
C 79	8	28.6	9	1	US-09-989-789-2454	Sequence 2454, Appl
C 80	8	28.6	9	1	US-09-989-789-2454	Sequence 2454, Appl
C 81	8	28.6	9	1	US-09-989-789-2454	Sequence 2454, Appl
C 82	8	28.6	9	1	US-09-989-789-2454	Sequence 2454, Appl
C 83	8	28.6	9	1	US-09-989-789-2454	Sequence 2454, Appl
C 84	8	28.6	9	1	US-09-989-789-2454	Sequence 2454, Appl
C 85	8	28.6	9	1	US-09-989-789-2454	Sequence 2454, Appl
C 86	8	28.6	9	1	US-09-989-789-2454	Sequence 2454, Appl
C 87	8	28.6	9	1	US-09-989-789-2454	Sequence 2454, Appl
C 88	8	28.6	9	1	US-09-989-789-2454	Sequence 2454, Appl
C 89	8	28.6	9	1	US-09-989-789-2454	Sequence 2454, Appl
C 90	8	28.6	9	1	US-09-989-789-2454	Sequence 2454, Appl
C 91	7.8	27.9	11	1	US-10-027-632-176254	Sequence 176254, Appl
C 92	7.8	27.9	11	1	US-10-027-632-176254	Sequence 176254, Appl
C 93	7.8	27.9	11	1	US-10-027-632-176254	Sequence 176254, Appl
C 94	7.8	27.9	11	1	US-10-027-632-176254	Sequence 176254, Appl
C 95	7.8	27.9	11	1	US-10-027-632-176254	Sequence 176254, Appl
C 96	7.8	27.9	11	1	US-10-027-632-176254	Sequence 176254, Appl
C 97	7.8	27.9	11	1	US-10-027-632-176254	Sequence 176254, Appl
C 98	7.8	27.9	11	1	US-10-027-632-176254	Sequence 176254, Appl
C 99	7.8	27.9	11	1	US-10-027-632-176254	Sequence 176254, Appl
C 100	7.8	27.9	11	1	US-10-027-632-176254	Sequence 176254, Appl
C 101	7.6	27.1	15	1	US-09-912-673A-55	Sequence 55, Appl
C 102	7.6	27.1	15	1	US-09-912-673A-55	Sequence 55, Appl
C 103	7.6	27.1	15	1	US-09-912-673A-55	Sequence 55, Appl
C 104	7.6	27.1	15	1	US-09-912-673A-55	Sequence 55, Appl
C 105	7.6	27.1	15	1	US-09-912-673A-55	Sequence 55, Appl
C 106	7.6	27.1	15	1	US-09-912-673A-55	Sequence 55, Appl

Sequence 2951, Ap
Sequence 73, Appl
Sequence 73, Appl
Sequence 319, Appl
Sequence 319, Appl
Sequence 319, Appl
Sequence 105, Appl
Sequence 105, Appl
Sequence 275, Appl
Sequence 19, Appl
Sequence 164, Appl
Sequence 203, Appl
Sequence 643, Appl
Sequence 1045, Ap
Sequence 1120, Ap
Sequence 643, Appl
Sequence 1045, Ap
Sequence 1120, Ap
Sequence 176254,
Sequence 176254,
Sequence 20, Appl
Sequence 2453, Ap
Sequence 2454, Ap
Sequence 2453, Ap
Sequence 2454, Ap
Sequence 2453, Ap
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Sequence 2454, Ap

107 7.6 27.1 17 1 US-10-261-185-2951
108 7.2 25.7 15 1 US-09-579-813-73
109 7.2 25.7 15 1 US-10-146-505-73
110 7.2 25.7 15 1 US-09-504-231A-319
111 7.2 25.7 15 1 US-09-274-553D-319
112 7.2 25.7 20 1 US-10-159-856-39
113 7.2 25.7 20 1 US-10-159-856-105
114 7 25.0 17 1 US-09-882-945A-275
115 6.8 24.3 12 1 US-09-929-507-19
116 6.8 24.3 14 1 US-08-591-486B-164
117 6.8 24.3 19 1 US-08-983-605-203
118 6.6 23.6 17 1 US-09-930-423-643
119 6.6 23.6 17 1 US-09-930-423-1045
120 6.6 23.6 17 1 US-09-930-423-1120
121 6.6 23.6 17 1 US-09-745-237A-643
122 6.6 23.6 17 1 US-09-745-237A-1045
123 6.6 23.6 17 1 US-09-745-237A-1120
124 6.4 22.9 11 1 US-10-027-632-176254
125 6.4 22.9 11 1 US-10-027-632-176254
126 6.2 22.1 12 1 US-10-407-637-20
127 6 21.4 9 1 US-09-989-789-2453
128 6 21.4 9 1 US-09-989-789-2454
129 6 21.4 9 1 US-09-990-186-2453
130 6 21.4 9 1 US-09-990-186-2454
131 6 21.4 9 1 US-09-989-994-2453
132 6 21.4 9 1 US-09-989-994-2454

ALIGNMENTS

RESULT 1
US-10-024-396-19/c
; Sequence 19, Application US/10024396
; Publication No. US20030147864A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD36L1 EXPRESSION
; FILE REFERENCE: RTS-0339
; CURRENT APPLICATION NUMBER: US/10/024,396
; CURRENT FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-024-396-19

Query Match 71.4%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCCTACGTGTACAGG 20
Db 20 CGGGCCCTACGTGTACAGG 1

RESULT 2
US-10-024-396-20/c
; Sequence 20, Application US/10024396
; Publication No. US20030147864A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD36L1 EXPRESSION
; FILE REFERENCE: RTS-0339
; CURRENT APPLICATION NUMBER: US/10/024,396
; CURRENT FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-024-396-20

Query Match 71.4%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ACGGTACAGGAGTCCAGG 28
Db 20 ACGGTACAGGAGTCCAGG 1

RESULT 3
US-08-983-605-203/c
; Sequence 203, Application US/08983605A
; Publication No. US20020066118A1
; GENERAL INFORMATION:
; APPLICANT: Roder, Marion
; TITLE OF INVENTION: Microsatellite Markers for Plants of the Species
; TITLE OF INVENTION: Triticum Aestivum and Tribe Triticeae and the Use of
; TITLE OF INVENTION: Said Markers
; FILE REFERENCE: 2936.10400
; CURRENT APPLICATION NUMBER: US/08/983,605A
; CURRENT FILING DATE: 1998-05-01
; EARLIER APPLICATION NUMBER: DE 195 25 284.5
; EARLIER FILING DATE: 1995-06-28
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 203
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-08-983-605-203

Query Match 50.7%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 5;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCCCTACGTGTACAGGGAG 22
Db 19 GCCTTAGCGGTACAGGGAG 1

RESULT 4
US-09-853-105-19
; Sequence 19, Application US/09853105
; Publication No. US20030149236A1
; GENERAL INFORMATION:
; APPLICANT: Hilton, Douglas J.
; TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/853,105
; FILING DATE: 10-May-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,665
; FILING DATE: 20-DEC-1996
; ATTORNEY/AGENT INFORMATION:

NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 10296
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 203 901 SANS UR
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-853-105-19

Query Match 50.7%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 6.1;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGGTACAGGAGTCCAGG 28
DB 3 CCTGACTGGAGTCCAGG 21

RESULT 5

US-09-918-779-35/c
Sequence 35, Application US/09918779
Publication No. US20030064369A1

GENERAL INFORMATION:
APPLICANT: Taupier, Raymond
APPLICANT: Padigaru, Muralidhara
APPLICANT: Rastelli, Luca
APPLICANT: Spaderma, Steven
APPLICANT: Shinkets, Richard
APPLICANT: Zerhusen, Bryan
APPLICANT: Spytek, Kimberly
APPLICANT: Shency, Suresh
APPLICANT: Li, Li
APPLICANT: Gusev, Vladimir
APPLICANT: Grosse, William
APPLICANT: Alsobrook, John
APPLICANT: Lepley, Denise
APPLICANT: Burgess, Catherine
APPLICANT: Gerlach, Valerie
APPLICANT: Ellerman, Karen
APPLICANT: MacDougall, John
APPLICANT: Stone, David
APPLICANT: Smithson, Glenda
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-074 US
CURRENT APPLICATION NUMBER: US/09/918,779
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/221,409
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/222,840
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,752
PRIOR FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/223,762
PRIOR FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/223,770
PRIOR FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/223,769
PRIOR FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/225,146
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/225,392
PRIOR FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: 60/225,470
PRIOR FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: 60/225,697

PRIOR FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: 60/263,862
PRIOR FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 60/281,645
PRIOR FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Oligonucleotide
OTHER INFORMATION: primers
US-09-918-779-35

Query Match 47.9%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 8.5;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 TACAGGAGTCCAGG 28
DB 17 TAGAGGAGTCCAGG 3

RESULT 6

US-10-159-856-39/c
Sequence 39, Application US/10159856
Publication No. US20030228689A1

GENERAL INFORMATION:
APPLICANT: Susan M. Freier
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPI
FILE REFERENCE: RTS-0365
CURRENT APPLICATION NUMBER: US/10/159,856
CURRENT FILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 134
SEQ ID NO 39
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-159-856-39

Query Match 47.1%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 9.4;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCCCTAGTGTACAGGGA 21
DB 19 GCGCATCGTGTACAGGGA 2

RESULT 7

US-10-159-856-105
Sequence 105, Application US/10159856
Publication No. US20030228689A1

GENERAL INFORMATION:
APPLICANT: Susan M. Freier
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPI
FILE REFERENCE: RTS-0365
CURRENT APPLICATION NUMBER: US/10/159,856
CURRENT FILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 134
SEQ ID NO 105
LENGTH: 20
TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
US-10-159-856-105


```
Query Match      47.1%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 9.4;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  4  GCCCTACGTGTACAGGGA 21
DB  2  GCGCATCGTGTACAGGGA 19

RESULT 8
US-10-184-372-23
; Sequence 23, Application US/10184372
; Publication No. US20030219852A1
; GENERAL INFORMATION:
; APPLICANT: Bank, Rudolf A.
; APPLICANT: Van der Slot, Annemarie J.
; APPLICANT: Zuurmond, Anne-Marie
; APPLICANT: Te Koppelaar, Johannes M.
; TITLE OF INVENTION: Modification of collagenous materials and medical treatment, diag
; TITLE OF INVENTION: and monitoring of fibrotic conditions
; FILE REFERENCE: P60187US00
; CURRENT APPLICATION NUMBER: US/10/184,372
; CURRENT FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: US 09/450,209
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-184-372-23

Query Match      44.3%; Score 12.4; DB 1; Length 19;
Best Local Similarity 92.9%; Pred. No. 13;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  15  ACAGGGAGTCCAGG 28
DB  3  ACAGGGATCCAGG 16

RESULT 9
US-09-882-945A-275
; Sequence 275, Application US/09882945A
; Publication No. US20030143535A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/09/882,945A
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 275
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-882-945A-275

Query Match      43.6%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 12;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2  GGCCCTACGTGTACAG 18
```

```
DB  1  GGACCTATGTCTACAG 17

RESULT 10
US-09-930-423-643/c
; Sequence 643, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBHB00,918-A,400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 643
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-643

Query Match      40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 18;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  11  GTGTACAGCGAGT 23
DB  15  GTGTACAGCGAGT 3

RESULT 11
US-09-930-423-1045/c
; Sequence 1045, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBHB00,918-A,400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1045
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1045

Query Match      40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 18;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  11  GTGTACAGCGAGT 23
DB  17  GTGTACAGCGAGT 5

RESULT 12
US-09-930-423-1120/c
; Sequence 1120, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBHB00,918-A,400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
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; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1120
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1120

Query Match          40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 18;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GTGTACAGCGAGT 23
Db 14 GTGTACAGCGAGT 2

RESULT 13
US-09-745-237A-643/c
; Sequence 643, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 643
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-643

Query Match          40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 18;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GTGTACAGCGAGT 23
Db 15 GTGTACAGCGAGT 3

RESULT 14
US-09-745-237A-1045/c
; Sequence 1045, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1045
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-1045

Query Match          40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 18;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GTGTACAGCGAGT 23
Db 15 GTGTACAGCGAGT 3

RESULT 15
US-09-745-237A-1120/c
; Sequence 1120, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1120
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-1120

Query Match          40.7%; Score 11.4; DB 1; Length 17;
Best Local Similarity 92.3%; Pred. No. 18;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GTGTACAGCGAGT 23
Db 14 GTGTACAGCGAGT 2

RESULT 16
US-09-818-875-2950/c
; Sequence 2950, Application US/09818875
; Publication No. US20030051270A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamber, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2950
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-818-875-2950

Query Match          40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 20;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 ACGTGTACAGCGAGTC 24
Db 17 ACTGTCCAGGAGGC 2

RESULT 17
US-09-818-875-2951
; Sequence 2951, Application US/09818875

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; Publication No. US20030051270A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2951
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-818-875-2951

Query Match 40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 20;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 ACGTGTACAGGAGTC 24
   |||||
Db 1 ACTTGTCCAGGAGGC 16

RESULT 18
US-10-156-306-7026
; Sequence 7026, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7026
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-156-306-7026

Query Match 40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 20;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 12 TGTACAGGGAGTCCAG 27
   :|||:
Db 2 UGCAGAGGAGUACAG 17

RESULT 19
US-10-156-306-7027
; Sequence 7027, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7026
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-156-306-7026

Query Match 40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 20;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 12 TGTACAGGGAGTCCAG 27
   :|||:
Db 2 UGCAGAGGAGUACAG 17

RESULT 20
US-10-238-700-3087
; Sequence 3087, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Lev
; FILE REFERENCE: 400/057 (MBH01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3087
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-238-700-3087

Query Match 40.0%; Score 11.2; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 CTACGTGTACAGGAG 22
   |||||
Db 1 CCACCAGACAGGAG 16

RESULT 21
US-10-209-787-2950/c
; Sequence 2950, Application US/10209787
; Publication No. US20030217377A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/10/209,787
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
```

; PRIOR APPLICATION NUMBER: US 60/244,989
 ; PRIOR FILING DATE: 2000-10-30
 ; NUMBER OF SEQ ID NOS: 4385
 ; SOFTWARE: Friedman macro Napro4
 ; SEQ ID NO 2950
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-209-787-2950

Query Match 40.0%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 20;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 ACGTGTACAGGAGTC 24
 |||||
 Db 17 ACTTGTCAGGAGGC 2

RESULT 22
 US-10-209-787-2951
 ; Sequence 2951, Application US/10209787
 ; Publication No. US20030217377A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kmiec, Eric B.
 ; APPLICANT: Gamper, Howard B.
 ; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
 ; FILE REFERENCE: Napro-4
 ; CURRENT APPLICATION NUMBER: US/10/209,787
 ; CURRENT FILING DATE: 2002-07-30
 ; PRIOR APPLICATION NUMBER: US 09/818,875
 ; PRIOR FILING DATE: 2001-03-27
 ; PRIOR APPLICATION NUMBER: US 60/192,176
 ; PRIOR FILING DATE: 2000-03-27
 ; PRIOR APPLICATION NUMBER: US 60/192,179
 ; PRIOR FILING DATE: 2000-03-27
 ; PRIOR APPLICATION NUMBER: US 60/208,538
 ; PRIOR FILING DATE: 2000-06-01
 ; PRIOR APPLICATION NUMBER: US 60/244,989
 ; PRIOR FILING DATE: 2000-10-30
 ; NUMBER OF SEQ ID NOS: 4385
 ; SOFTWARE: Friedman macro Napro4
 ; SEQ ID NO 2951
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-209-787-2951

Query Match 40.0%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 20;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 ACGTGTACAGGAGTC 24
 |||||
 Db 1 ACTTGTCAGGAGGC 16

RESULT 23
 US-10-261-185-2950/c
 ; Sequence 2950, Application US/10261185
 ; Publication No. US20040014057A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kmiec, Eric B.
 ; APPLICANT: Gamper, Howard B.
 ; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
 ; FILE REFERENCE: Napro-4CON
 ; CURRENT APPLICATION NUMBER: US/10/261,185
 ; CURRENT FILING DATE: 2002-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/09761

; PRIOR FILING DATE: 2001-03-27
 ; PRIOR APPLICATION NUMBER: US 60/192,176
 ; PRIOR FILING DATE: 2000-03-27
 ; PRIOR APPLICATION NUMBER: US 60/192,179
 ; PRIOR FILING DATE: 2000-03-27
 ; PRIOR APPLICATION NUMBER: US 60/208,538
 ; PRIOR FILING DATE: 2000-06-01
 ; PRIOR APPLICATION NUMBER: US 60/244,989
 ; NUMBER OF SEQ ID NOS: 4385
 ; SOFTWARE: Friedman macro Napro4
 ; SEQ ID NO 2950
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-261-185-2950

Query Match 40.0%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 20;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 ACGTGTACAGGAGTC 24
 |||||
 Db 17 ACTTGTCAGGAGGC 2

RESULT 24
 US-10-261-185-2951
 ; Sequence 2951, Application US/10261185
 ; Publication No. US20040014057A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kmiec, Eric B.
 ; APPLICANT: Gamper, Howard B.
 ; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
 ; FILE REFERENCE: Napro-4CON
 ; CURRENT APPLICATION NUMBER: US/10/261,185
 ; CURRENT FILING DATE: 2002-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/09761
 ; PRIOR FILING DATE: 2001-03-27
 ; PRIOR APPLICATION NUMBER: US 60/192,176
 ; PRIOR FILING DATE: 2000-03-27
 ; PRIOR APPLICATION NUMBER: US 60/192,179
 ; PRIOR FILING DATE: 2000-03-27
 ; PRIOR APPLICATION NUMBER: US 60/208,538
 ; PRIOR FILING DATE: 2000-06-01
 ; PRIOR APPLICATION NUMBER: US 60/244,989
 ; NUMBER OF SEQ ID NOS: 4385
 ; SOFTWARE: Friedman macro Napro4
 ; SEQ ID NO 2951
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-261-185-2951

Query Match 40.0%; Score 11.2; DB 1; Length 17;
 Best Local Similarity 81.2%; Pred. No. 20;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 ACGTGTACAGGAGTC 24
 |||||
 Db 1 ACTTGTCAGGAGGC 16

RESULT 25
 US-09-504-231A-143
 ; Sequence 143, Application US/09504231A
 ; Patent No. US20020013458A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Blatt, Lawrence
 ; APPLICANT: McSwiggen, James

APPLICANT: Roberts, Beth
APPLICANT: Pavco, Pamela
APPLICANT: Macejak, Dennis
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
FILE REFERENCE: fpi 247/282
CURRENT APPLICATION NUMBER: US/09/504,231A
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 09/274,553
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 09/257,608
PRIOR FILING DATE: 1999-02-24
PRIOR APPLICATION NUMBER: 60/100,842
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/083,217
PRIOR FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 3.0
SOFTWARE: PatentIn version 3.0
SEQ ID NO 143
LENGTH: 15
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-143

Query Match 38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 19;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCCCTACGTGTA 15
|||||: |||:
DB 1 GGGCCCUCCUGCA 14

RESULT 26
US-09-274-553D-143
Sequence 143, Application US/09274553D
Patent No. US20020082225A1
GENERAL INFORMATION:
APPLICANT: McSwiggen, James
APPLICANT: Roberts, Beth
APPLICANT: Pavco, Pamela
APPLICANT: Macejak, Dennis
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
FILE REFERENCE: fpi 247/282
CURRENT APPLICATION NUMBER: US/09/274,553D
CURRENT FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 09/257,608
PRIOR FILING DATE: 1999-02-24
PRIOR APPLICATION NUMBER: 60/100,842
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/083,217
PRIOR FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 3.148
SOFTWARE: PatentIn version 3.0
SEQ ID NO 143
LENGTH: 15
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-143

Query Match 38.6%; Score 10.8; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 19;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGCCCTACGTGTA 15
|||||: |||:
DB 1 GGGCCCUCCUGCA 14

RESULT 27
US-10-407-637-20/c
Sequence 20, Application US/10407637
Publication No. US20030194736A1
GENERAL INFORMATION:
APPLICANT: Bitinaite, Jurate
TITLE OF INVENTION: Methods And Compositions For DNA Manipulation
FILE REFERENCE: NEB-203-US
CURRENT APPLICATION NUMBER: US/10/407,637
CURRENT FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: US 60/372,352
PRIOR FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US 60/372,675
PRIOR FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 60/421,010
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.2
SEQ ID NO 20
LENGTH: 12
TYPE: DNA
ORGANISM: unknown
FEATURE:
OTHER INFORMATION: mutated pUC19
US-10-407-637-20

Query Match 37.1%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 15;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCTACGTGTACA 17
|||||: |||:
DB 12 CCTAGGTGTACA 1

RESULT 28
US-09-879-813-73/c
Sequence 73, Application US/09879813
Patent No. US20020155453A1
GENERAL INFORMATION:
APPLICANT: Neuberger, Michael S.
APPLICANT: Cumbers, Sarah J.
TITLE OF INVENTION: Method of Generating Diversity
FILE REFERENCE: 18396/2005
CURRENT APPLICATION NUMBER: US/09/879,813
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 09/828,717
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: PCT/GB99/03358
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn version 3.1
SEQ ID NO 73
LENGTH: 15
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (7)..(10)
OTHER INFORMATION: F264
OTHER INFORMATION: The sequence ACA replaces the sequence GAGAG.46bp.CGTC
US-09-879-813-73

Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 26;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GGCCTACGTGTACAG 18
|||||: |||:
DB 15 GGCCTACGTGTACAG 1

RESULT 29
US-09-912-673A-55/c
; Sequence 55, Application US/09912673A
; Publication No. US20030186230A1
; GENERAL INFORMATION:
; APPLICANT: Ye, Bangce
; TITLE OF INVENTION: MEDIUM AND LOW DENSITY GENE CHIPS
; FILE REFERENCE: JNB 100
; CURRENT APPLICATION NUMBER: US/09/912,673A
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 15
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: P(qs)1 DNA probe
US-09-912-673A-55

Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 26;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CGTGTACAGGGAGTC 24
DB 15 CTGTCCAGGGAGGC 1

RESULT 30
US-10-146-505-73/c
; Sequence 73, Application US/10146505
; Publication No. US20030108869A1
; GENERAL INFORMATION:
; APPLICANT: Neuberger, Michael S.
; APPLICANT: Cumbers, Sarah J.
; TITLE OF INVENTION: Method of Generating Diversity
; FILE REFERENCE: 18396/2005B
; CURRENT APPLICATION NUMBER: US/10/146,505
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/828,717
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 09/879,813
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: PCT/GB99/03358
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: GB 9822104.7
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: GB 9901141.3
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: GB 9913435.5
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)..(10)
; OTHER INFORMATION: F264
; OTHER INFORMATION: The sequence ACA replaces the sequence GAGAG.46bp.COTC
US-10-146-505-73

Query Match 36.4%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 26;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCCTACGTGTACAG 18

DB 15 GCCCATGTGCACAG 1

RESULT 31
US-10-193-507-83
; Sequence 83, Application US/10193507
; Publication No. US20040018493A1
; GENERAL INFORMATION:
; APPLICANT: Anastasio, Alison E.
; APPLICANT: Kazemi, Amir
; APPLICANT: Lachowicz, Michael F.
; APPLICANT: Pabon, Vicente
; APPLICANT: Shah, Nisha
; TITLE OF INVENTION: HAPLOTYPES OF THE CD3E GENE
; FILE REFERENCE: MMH-2790US
; CURRENT APPLICATION NUMBER: US/10/193,507
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 60/304,573
; PRIOR FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-193-507-83

Query Match 35.7%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 ACAGGGAGTC 24
DB 1 ACAGGGAGTC 10

RESULT 32
US-09-504-231A-319
; Sequence 319, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELA
; FILE REFERENCE: FPI 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 319
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-319

Query Match 35.7%; Score 10; DB 1; Length 15;
Best Local Similarity 90.0%; Pred. No. 29;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGAGTCCAGG 28
|||||
Db 3 GGAGUCCAGG 12

RESULT 33

US-09-274-553D-319
; Sequence 319, Application US/09274553D
; Patent No. US2002008225A1

GENERAL INFORMATION:

; APPLICANT: Blatt, Lawrence

; APPLICANT: McSwiggan, James

; APPLICANT: Roberts, Beth

; APPLICANT: Pavco, Pamela

; APPLICANT: MacGjak, Dennis

; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE

; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION

; FILE REFERENCE: IPI 247/282

; CURRENT APPLICATION NUMBER: US/09/274,553D

; CURRENT FILING DATE: 1999-03-23

; PRIOR APPLICATION NUMBER: 09/257,608

; PRIOR FILING DATE: 1999-02-24

; PRIOR APPLICATION NUMBER: 60/100,842

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: 60/083,217

; PRIOR FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 3148

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 319

; LENGTH: 15

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target

US-09-274-553D-319

Query Match 35.7%; Score 10; DB 1; Length 15;
Best Local Similarity 90.0%; Pred. No. 29;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 19 GGAGTCCAGG 28
|||||
Db 3 GGAGUCCAGG 12

RESULT 34

US-10-193-507-51

; Sequence 51, Application US/10193507

; Publication No. US20040018493A1

GENERAL INFORMATION:

; APPLICANT: Anastasio, Alison E.

; APPLICANT: Kazemi, Amir

; APPLICANT: Lachowicz, Michael F.

; APPLICANT: Pabon, Vicente

; APPLICANT: Shah, Nisha

; TITLE OF INVENTION: HAPLOTYPES OF THE CD3E GENE

; FILE REFERENCE: MWH-2790US

; CURRENT APPLICATION NUMBER: US/10/193,507

; CURRENT FILING DATE: 2002-07-12

; PRIOR APPLICATION NUMBER: 60/304,573

; PRIOR FILING DATE: 2001-07-11

; NUMBER OF SEQ ID NOS: 86

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 51

; LENGTH: 15

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-193-507-51

Query Match 35.7%; Score 10; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 ACAGGGAGTC 24
|||||
Db 4 ACAGGGAGTC 13

RESULT 35

US-08-591-486B-61

; Sequence 61, Application US/08591486B

; Publication No. US20020037866A1

GENERAL INFORMATION:

; APPLICANT: Schlingensiepen, Georg F

; APPLICANT: Schlingensiepen, Reimar

; APPLICANT: Gottingen, Wolfgang Brysch

; TITLE OF INVENTION: A Pharmaceutical Composition

; TITLE OF INVENTION: Comprising Antisense-Nucleic Acid for Prevention and/or Treat

; TITLE OF INVENTION: of Neuronal Injury, Degeneration and Cell Death and for the

; TITLE OF INVENTION: Treatment of Neoplasms

; NUMBER OF SEQUENCES: 185

; CORRESPONDENCE ADDRESS: 185

; ADDRESSEE: Jacobson, Price, Holman & Stern

; STREET: 400 Seventh Street, N.W.

; CITY: Washington, D.C.

; COUNTRY: U.S.A.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/591,486B

; FILING DATE: 11-JAN-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 93111059.7

; FILING DATE: 10-JUL-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/EP94/02218

; FILING DATE: 6-JUL-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Player, William E.

; REGISTRATION NUMBER: 31,409

; REFERENCE/DOCKET NUMBER: 10496/P60122

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 638-6666

; TELEFAX: (202) 393-9350

; TELEX: RCA 248593 IDEA UR

; INFORMATION FOR SEQ ID NO: 61:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 14 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: DNA (genomic)

; ANTI-SENSE: YES

US-08-591-486B-61

Query Match 35.0%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CGGTGACAGGAG 22
|||||
Db 2 CGGTGACAGGAG 14

RESULT 36

US-09-504-231A-137

; Sequence 137, Application US/09504231A

; Patent No. US20020013459A1

GENERAL INFORMATION:

```
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: IPI 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 137
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target.
US-09-504-231A-137

Query Match          35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 32;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      3  GGCCCTACGTGTA 15
      |||||:|:|:|
Db      2  GGCCCUACGUUA 14

RESULT 37
US-09-274-553D-137
; Sequence 137, Application US/09274553D
; Patent No. US2002008225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: IPI 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 137
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-137

Query Match          35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 61.5%; Pred. No. 32;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      3  GGCCCTACGTGTA 15
      |||||:|:|:|
Db      2  GGCCCUACGUUA 14

RESULT 38
US-10-113-877-35
; Sequence 35, Application US/10113877
; Publication No. US20020177218A1
; GENERAL INFORMATION:
; APPLICANT: Fang, Yu
; APPLICANT: Wang, Xiao-Yang
; APPLICANT: Turpin, Pierre
; TITLE OF INVENTION: Methods of detecting multiple DNA
; TITLE OF INVENTION: Binding protein and DNA interactions in a sample, and
; TITLE OF INVENTION: devices, systems and kits for practicing the same.
; FILE REFERENCE: CLON-071
; CURRENT APPLICATION NUMBER: US/10/113,877
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 60/280,658
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/314,330
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-113-877-35

Query Match          35.0%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 32;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      13  GTACAGGGAGTCC 25
      |||||:|:|:|
Db      2  GTACAGGGGTGTC 14

RESULT 39
US-09-989-364-67
; Sequence 67, Application US/09989364
; Publication No. US2003003463A1
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan M
; APPLICANT: Nallur, Girish N
; APPLICANT: Hu, Xinghua
; TITLE OF INVENTION: Methods and Devices for Measuring
; TITLE OF INVENTION: Differential Gene Expression
; FILE REFERENCE: 7934-052
; CURRENT APPLICATION NUMBER: US/09/989,364
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/203,231
; PRIOR FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-989-364-67

Query Match          33.6%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 26;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6  CCTACGTGTAC 16
      |||||:|:|:|
Db      2  CCTACCTGTAC 12
```


RESULT 40
US-08-591-486B-164/c
; Sequence 164, Application US/08591486B
; Publication No. US20020037866A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg F
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Göttingen, Wolfgang Brysch
; TITLE OF INVENTION: A Pharmaceutical Composition
; TITLE OF INVENTION: Comprising Antisense-Nucleic Acid for Prevention and/or Treatment
; TITLE OF INVENTION: Of Neuronal Injury, Degeneration and Cell Death and for the
; TITLE OF INVENTION: Treatment of Neoplasms
; NUMBER OF SEQUENCES: 185
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,486B
; FILING DATE: 11-JAN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93111059.7
; FILING DATE: 10-JUL-1993
; PRIOR APPLICATION DATA: PCT/EP94/02218
; FILING DATE: 6-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10496/P60122
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-9350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-591-486B-164

Query Match 32.9%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 38;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 CCTACGTGTACAGG 19
DB 14 CCTCTGTATACAGG 1

RESULT 41
US-10-330-627-29
; Sequence 29, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes

FILE REFERENCE: 001107.00319
CURRENT APPLICATION NUMBER: US/10/330,627
CURRENT FILING DATE: 2002-12-30
PRIOR APPLICATION NUMBER: US 09/448,480
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 1564
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 29
LENGTH: 10
TYPE: DNA
ORGANISM: Homo sapiens
US-10-330-627-29

Query Match 32.1%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 GAGTCCAGG 28
DB 2 GAGTCCAGG 10

RESULT 42
US-09-989-364-67/c
; Sequence 67, Application US/09989364
; Publication No. US20030003463A1
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan M
; APPLICANT: Nallur, Girish N
; APPLICANT: Hu, Xinghua
; TITLE OF INVENTION: Methods and Devices for Measuring
; TITLE OF INVENTION: Differential Gene Expression
; FILE REFERENCE: 7934-052
CURRENT APPLICATION NUMBER: US/09/989,364
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 09/203,231
PRIOR FILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 67
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-989-364-67

Query Match 31.4%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 GTACAGGGAGTC 24
DB 12 GTACAGGTAGGC 1

RESULT 43
US-10-104-307-26
; Sequence 26, Application US/10104307
; Publication No. US20030180729A1
; GENERAL INFORMATION:
; APPLICANT: GUNNING, Kerry B.
; APPLICANT: POWDRILL, Tom
; APPLICANT: HOGAN, Michael
; TITLE OF INVENTION: Hybridization Rate Enhancement for Substrate-Bound Specific Nuc
; TITLE OF INVENTION: Binding Agents
; FILE REFERENCE: 053960.0001/AUS
CURRENT APPLICATION NUMBER: US/10/104,307
CURRENT FILING DATE: 2002-03-22
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.0
SEQ ID NO 26
LENGTH: 13

```
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)-(13)
/ OTHER INFORMATION: synthetic oligonucleotide
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(1)
/ OTHER INFORMATION: 5' amine modification
US-10-104-307-26
```

```
Query Match 31.4%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 40;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 12 TGTACAGGGAGT 23
    |||||
Db 2 TGTACAGGGCGT 13
```

RESULT 44

```
US-09-851-871-85/c
/ Sequence 85, Application US/09851871
/ Publication No. US20030176374A1
/ GENERAL INFORMATION:
/ APPLICANT: Bennett, Clarence Frank
/ APPLICANT: Vickers, Timothy A.
/ APPLICANT: Karras, James G.
/ TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
/ FILE REFERENCE: ISPH-0543
/ CURRENT APPLICATION NUMBER: US/09/851,871
/ PRIOR FILING DATE: 2001-05-09
/ PRIOR APPLICATION NUMBER: PCT/US00/14471
/ PRIOR FILING DATE: 2000-05-25
/ PRIOR APPLICATION NUMBER: 09/326,186
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: 08/777,266
/ PRIOR FILING DATE: 1996-12-31
/ NUMBER OF SEQ ID NOS: 284
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 85
/ LENGTH: 10
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic
US-09-851-871-85
```

```
Query Match 30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 31;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 13 GTACAGGGAG 22
    |||||
Db 10 GTACGGGGAG 1
```

RESULT 45

```
US-10-329-465-242/c
/ Sequence 242, Application US/10329465
/ Publication No. US20030165949A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang et al.
/ TITLE OF INVENTION: GENES ABNORMALLY EXPRESSED IN MYELOID LEUKEMIA CELLS WITH AN MLL-
/ FILE REFERENCE: 27373/37928A
/ CURRENT APPLICATION NUMBER: US/10/329,465
/ CURRENT FILING DATE: 2002-12-23
/ PRIOR APPLICATION NUMBER: US 60/343,826
/ PRIOR FILING DATE: 2001-12-27
/ NUMBER OF SEQ ID NOS: 315
/ SOFTWARE: PatentIn version 3.1
```

```
/ SEQ ID NO 242
/ LENGTH: 10
/ TYPE: DNA
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic oligonucleotide
US-10-329-465-242
```

```
Query Match 30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 31;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 12 TGTACAGGGA 21
    |||||
Db 10 TGTACGGGGA 1
```

RESULT 46

```
US-10-390-045-14
/ Sequence 14, Application US/10390045
/ Publication No. US20030170713A1
/ GENERAL INFORMATION:
/ APPLICANT: SRIVASTAVA, SHIV
/ APPLICANT: MOUL, JUDD W.
/ APPLICANT: XU, LINDA L.
/ APPLICANT: SEGAWA, TAKEHIKO
/ TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
/ FILE REFERENCE: 04995.0057-00000
/ CURRENT APPLICATION NUMBER: US/10/390,045
/ CURRENT FILING DATE: 2003-03-18
/ PRIOR APPLICATION NUMBER: US/09/769,482
/ PRIOR FILING DATE: 2001-01-26
/ PRIOR APPLICATION NUMBER: 60/178,772
/ PRIOR FILING DATE: 2000-01-28
/ PRIOR APPLICATION NUMBER: 60/179,045
/ PRIOR FILING DATE: 2000-01-31
/ NUMBER OF SEQ ID NOS: 67
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 14
/ LENGTH: 10
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: oligonucleotide
US-10-390-045-14
```

```
Query Match 30.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 31;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 13 GTACAGGGAG 22
    |||||
Db 1 GTGCAGGGAG 10
```

RESULT 47

```
US-10-330-627-1257/c
/ Sequence 1257, Application US/10330627
/ Publication No. US2003017571A1
/ GENERAL INFORMATION:
/ APPLICANT: Velculescu, Victor E.
/ APPLICANT: Kinzler, Kenneth W.
/ APPLICANT: Vogelstein, Bert
/ TITLE OF INVENTION: Human Transcriptomes
/ FILE REFERENCE: 001107.00319
/ CURRENT APPLICATION NUMBER: US/10/330,627
/ CURRENT FILING DATE: 2002-12-30
/ PRIOR APPLICATION NUMBER: US 09/448,480
/ PRIOR FILING DATE: 1999-11-24
/ NUMBER OF SEQ ID NOS: 1584
/ SOFTWARE: FastSeq for Windows Version 4.0
```